

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:35:16 ; Search time 232 seconds

(without alignments)
964.019 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730

Sequence: 1 MRAAAAGGVRTALALLG.....MPSYPCSLYPPFYGAEPH 317

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1730	100.0	317	1 SFRP5_HUMAN	Q514F7 homo sapien
2	1656	95.7	315	1 SFRP5_BOVIN	Q9XCI1 bos taurus
3	1613	93.2	314	1 SFRP5_MOUSE	Q99J66 mus musculu
4	1160.5	67.1	315	2 Q6G150_XENTR	Q6G150 xenopus tro
5	1157.5	66.9	315	2 Q8AWG4_XENLA	Q8AWG4 xenopus lae
6	1155.5	66.8	315	2 Q640J3_XENLA	Q640J3 xenopus lae
7	1104.5	63.8	321	2 Q4SKC3_TETNG	Q4SKC3 tetraodon n
8	1089	62.9	310	2 Q6VNR8_BRARE	Q6VNR8 brachydanio
9	924.5	53.4	314	1 SFRP1_HUMAN	Q8N474 homo sapien
10	910.5	52.6	308	1 SFRP1_BOVIN	Q19116 bos taurus
11	909	52.5	314	2 Q505A2_MOUSE	Q505A2 mus musculu
12	903	52.2	314	1 SFRP1_MOUSE	Q8CAJ3 mus musculu
13	851	49.2	306	2 Q6GZK1_ORYLA	Q6GZK1 oryzae lat
14	838	48.4	314	1 SFRP1_CHICK	Q9D641 gallus gall
15	836.5	48.4	311	2 Q9Y124_XENLA	Q9Y124 xenopus lae
16	802	46.4	296	2 Q7TK9_BRARE	Q7TK9 brachydanio
17	783	45.3	281	2 Q568X0_BRARE	Q568X0 brachydanio
18	744	43.0	311	2 Q8JHC7_BRARE	Q8JHC7 brachydanio
19	712	41.2	282	2 Q8JHC7_BRARE	Q8JHC7 brachydanio
20	672	38.8	295	2 Q4SS00_TETNG	Q4SS00 tetraodon n
21	643	37.2	295	2 Q6PAB8_XENTR	Q6PAB8 xenopus tro
22	643	37.2	298	2 Q7ZKM6_XENLA	Q7ZKM6 xenopus lae
23	620.5	35.9	295	1 SFRP2_MOUSE	Q97299 mus musculu
24	617	35.7	294	1 SFRP2_CANFA	Q96311 canis famli
25	616	35.6	283	2 Q9BGS6_RABIT	Q9BGS6 oryctolagus
26	614.5	35.5	295	1 SFRP2_HUMAN	Q961F1 homo sapien
27	602	34.8	292	1 SFRP2_CHICK	Q91956 gallus gall
28	581	33.6	365	2 Q4R2U5_CIOIN	Q4R2U5 ciona intes
29	568.5	32.9	300	2 Q6FZB8_XENTR	Q6FZB8 xenopus tro
30	568	32.8	307	2 Q42397_CHICK	Q42397 gallus gall
31	564.5	32.6	295	2 Q91897_XENLA	Q91897 xenopus lae

32	490.5	28.4	293	2 Q4H2U4_CIOIN	Q4H2U4 ciona intes
33	473	27.3	115	2 Q90ZG8_BRARE	Q90ZG8 brachydanio
34	453	26.2	158	1 SFRP1_RAT	Q91168 ratcus norv
35	431	24.9	282	2 Q4RS17_TETNG	Q4RS17 tetraodon n
36	398	23.0	280	2 Q91AUS_XENLA	Q91AUS xenopus lae
37	396.5	22.9	261	2 Q61U61_CABBR	Q61U61 caenorhabdi
38	396	22.9	281	2 Q73821_XENLA	Q73821 xenopus lae
39	390.5	22.6	284	2 Q90ZAG_AMBME	Q90ZAG ambystoma m
40	388	22.4	260	2 Q9GUF5_CABEL	Q9GUF5 caenorhabdi
41	373	21.6	178	2 Q6ZSL4_HUMAN	Q6ZSL4 homo sapien
42	370.5	21.4	282	2 Q7SX78_BRARE	Q7SX78 brachydanio
43	370.5	21.4	289	2 Q504U9_BRARE	Q504U9 brachydanio
44	300	17.3	567	1 F2D7_CHICK	Q57329 gallus gall
45	292.5	16.9	574	1 F2D7_HUMAN	Q75084 homo sapien

ALIGNMENTS

RESULT 1
SFRP5_HUMAN STANDARD; PRT; 317 AA.
ID Q514F7, Q14780; Q86TH7;
AC 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Secreted frizzled-related protein 5 precursor (SFRP-5) (Secreted
DE apoptosis related protein 3) (SARP-3) (Frizzled-related protein 1b)
DE (FRP-1b).
GN Name=SFRP5; Synonyms=FRP1b, SARP3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=Pancreas;
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M.,
RA Fitzpatrick P.A., Kiefer M.C., Tomei L.D., Umanetsky S.R.;
RT "SARPs: a family of secreted apoptosis-related proteins.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX PubMed=9642118; DOI=10.1006/birc.1998.8784;
RA Hu B., Zhu Y., Fredrickson T., Barnes W., Kelsell D., Beeley L.,
RA Brooks D.;
RT "Tissue restricted expression of two human Frzbs in preadipocytes and
RT pancreas.";
RN Biochem. Biophys. Res. Commun. 247:287-293(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND TISSUE SPECIFICITY.
RC TISSUE=Retina;
RX PubMed=10072424; DOI=10.1093/hmg/8.4.575;
RA Chang J.T., Sami N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RN Hum. Mol. Genet. 8:575-583(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT GLY-7.
RC TISSUE=retal brain;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization.";
RN Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANT GLY-7.
RX PubMed=15164054; DOI=10.1038/nature02462;
RA Deloukas P., Barchrow M.E., Grahm D.V., Rubinfeld M., French L.,
RA Steward C.A., Sims S.K., Jones M.C., Seale S., Scott C., Howe K.,
RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA Taylor A., Battles J., Bird C.P., Alincough R., Almeida J.P.,

RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baguley C.L., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burton D.C., Burdill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhumi P., Dutta I., Dunn M., Faulkner L.,
 RA Griffiths A., Frankland J.A., Garner P., Garnett J., Gribble S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McIay K.B., McMurtry A.,
 RA Mshreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pellan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarafidou T., Sehra H.K., Showkhen R., Skuce C.D., Smith M.,
 RA Stauding L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Tsoles J., Wall M., Walsh J., Wang H.,
 RA Weinstein K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fochtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 10.";
 RT Nature 429:375-381 (2004).

RA [6]

RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RA TISSUE=BNS;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalcenon M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Parnce C.,
 RA Raha S.A., Loggellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Soluble frizzled-related proteins (SFRPs) function as
 CC modulators of Wnt signaling through direct interaction with Wnts.
 CC They have a role in regulating cell growth and differentiation in
 CC specific cell types. SFRPs may be involved in determining the
 CC polarity of photoreceptor, and perhaps, other cells in the retina.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in the retinal pigment
 CC epithelium (RPE) and pancreas. Weak expression in heart, liver and
 CC muscle.
 CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
 CC (SFRP) family.
 CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
 CC -1- SIMILARITY: Contains 1 NTR domain.

CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC DR EMBL, AF017988; AAB70294.1; -; mRNA.
 CC DR EMBL, AF017758; AAD25052.1; -; mRNA.
 CC DR EMBL, CR596705; -; NOT_ANNOTATED_CDS; mRNA.

DR EMBL, AL358938; CA114274.1; -; Genomic_DNA.
 DR EMBL, BC050435; AAH50435.2; -; mRNA.
 DR PIR, J010175; J010175.
 DR HSSP, Q61091; I1Y7.
 DR Ensembl, ENSG00000120057; Homo sapiens.
 DR HGNC, HGNC:10779; SFRP5.
 DR MIM, 604158; -; SFRP5.
 DR InterPro, IPR000024; Fz_domain.
 DR InterPro, IPR01134; Netrin_C.
 DR Pfam, PF01392; Fz; 1.
 DR Pfam, PF01759; NTR; 1.
 DR SMART, SM00643; NTR; 1.
 DR SMART, SM00063; FRI; 1.
 DR PROSITE, PS50038; FZ; 1.
 DR PROSITE, PS50189; NTR; 1.
 KW Developmental protein; Differentiation; Polymorphism; Signal;
 KW Wnt signaling pathway.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 317 Secreted frizzled-related protein 5.
 FT DOMAIN 48 165 FZ.
 FT DOMAIN 181 303 NTR.
 FT DISULFID 53 116 By similarity.
 FT DISULFID 63 109 By similarity.
 FT DISULFID 100 135 By similarity.
 FT DISULFID 124 162 By similarity.
 FT DISULFID 128 152 By similarity.
 FT DISULFID 181 255 By similarity.
 FT DISULFID 184 253 By similarity.
 FT DISULFID 198 303 By similarity.
 FT VARIANT 7 7 A->G (in dbSNP:11815012).
 FT VARIANT 7 7 /FTID=VAR_021412.
 FT CONFLICT 33 33 D->H (in Ref. 2).
 FT SQ SEQUENCE 317 AA; 35577 MW; 05F1FCCB614F36A CRC64;

Query Match 100.0%; Score 1730; DB 1; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.5e-149;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGAGVTRPALALLLGLAHMAPARCEEYDYGWQAEPLHGRSYSPQCLDIPADL 60
 DB 1 MRAAAGAGVTRPALALLLGLAHMAPARCEEYDYGWQAEPLHGRSYSPQCLDIPADL 60
 QY 61 PLCHTVGKRRRLPVLHESLAEVKQOASSWPLIARCSHSDTVFLCSLFAVPCIDLRP 120
 DB 61 PLCHTVGKRRRLPVLHESLAEVKQOASSWPLIARCSHSDTVFLCSLFAVPCIDLRP 120
 QY 121 IYPCSLCEAVRAGCAPLMEAYGFPMPMLCHKRPPLNDICIAVQFGLHPATAPVTKI 180
 DB 121 IYPCSLCEAVRAGCAPLMEAYGFPMPMLCHKRPPLNDICIAVQFGLHPATAPVTKI 180
 QY 181 CAOCMEHSADQLMEQWCSDFVVMRIKEIKIENGDRKLGAOKKKLLRGPDKRDT 240
 DB 181 CAOCMEHSADQLMEQWCSDFVVMRIKEIKIENGDRKLGAOKKKLLRGPDKRDT 240
 QY 241 KRLVLMKNGAGCCPQDLSLAGSLVNGRKYDQGLLMAVYRMDKXKXKFAVKFMPFS 300
 DB 241 KRLVLMKNGAGCCPQDLSLAGSLVNGRKYDQGLLMAVYRMDKXKXKFAVKFMPFS 300
 QY 301 YPCSLYPPFPYGAEPH 317
 DB 301 YPCSLYPPFPYGAEPH 317

RESULT 2
 SFRP5_BOVIN
 ID SFRP5_BOVIN STANDARD; PRT; 315 AA.
 AC Q9XSCI;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 GN Secreted frizzled-related protein 5 precursor (SFRP-5).
 GN Name=SFRP5.
 OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelosteomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA], AND TISSUE SPECIFICITY.
 RC TISSUE=retinal pigment epithelium;
 RC PubMed=10072424; DOI=10.1093/hmg/8.4.575;
 RA Chang J.T., Baum N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
 RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
 RT "Cloning and characterization of a secreted frizzled-related protein
 RT that is expressed by the retinal pigment epithelium.";
 RL Hum. Mol. Genet. 8:575-583(1999).
 CC -1- FUNCTION: Soluble frizzled-related proteins (sFRPs) function as
 CC modulators of Wnt signaling through direct interaction with Wnts.
 CC They have a role in regulating cell growth and differentiation in
 CC specific cell types. sFRPs may be involved in determining the
 CC polarity of photoreceptor, and perhaps other, cells in the retina.
 CC Inhibits Wnt8 signaling, in vitro.
 CC SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: Strongly expressed in the retinal pigment
 CC epithelium (RPE). Weak expression in retina, brain, heart, liver,
 CC kidney, testis and muscle.
 CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
 CC (sFRP) family.
 CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: AF117757; AAD25051.1; -; mRNA.
 DR HSSP: O61091; 11YI.
 DR InterPro: IPR000024; Fz domain.
 DR InterPro: IPR001134; Netlin_C.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF01759; NTR; 1.
 DR SMART: SM00643; C34SC; 1.
 DR SMART: SM00663; FRI; 1.
 DR PROSITE: PS50038; FZ; 1.
 DR PROSITE: PS50189; NTR; 1.
 KW Developmental protein; Differentiation; Signal; Wnt signaling pathway.
 FT SIGNAL 1 27
 FT CHAIN 28 315
 FT DOMAIN 163 301
 FT DOMAIN 179 301
 FT DISULFID 51 114
 FT DISULFID 61 107
 FT DISULFID 98 133
 FT DISULFID 122 160
 FT DISULFID 126 150
 FT DISULFID 179 253
 FT DISULFID 182 251
 FT DISULFID 196 301
 FT DISULFID 301
 SQ SEQUENCE 315 AA; 35279 MW; 886E94951060A976 CRC64;
 Query Match 95.7%; Score 1656; DB 1; Length 315;
 Best Local Similarity 97.4%; Pred. No. 8-5e-143;
 Matches 305; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 125 RSLCEAVRAGCAPLMEAYGFPMPEMLHCKEPLNDLCIAVQFGLPATAPPTIKCAQC 184
 DB 123 RSLCEAVRAGCAPLMEAYGFPMPEMLHCKEPLNDLCIAVQFGLPATAPPTIKCAQC 182
 QY 165 EMEHSADGLMOMCSDDVVKRIKEIKENGRDLIAQKKKLLKSGPLKRTKRLV 244
 DB 163 EMEHSADGLMOMCSDDVVKRIKEIKENGRDLIAQKKKLLKSGPLKRTKRLV 242
 QY 245 LHMKGAGCPCPQDLSLGSFLVMGRKYDGLLMAVVRMPDKNKMFAVYFMPSPCS 304
 DB 243 LHMKGAGCPCPQDLSLGSFLVMGRKYDGLLMAVVRMPDKNKMFAVYFMPSPCS 302
 QY 305 LYPPFYGAABPH 317
 DB 303 LYPPFYGAABPH 315
 RESULT 3
 ID SFRP5_MOUSE STANDARD; PRT; 314 AA.
 AC 09WU66; 08K269;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Secreted frizzled-related protein 5 precursor (sFRP-5).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelosteomi;
 OC Mammalia; Eutheria; Eucarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
 RC TISSUE=retina;
 RC PubMed=10072424; DOI=10.1093/hmg/8.4.575;
 RA Chang J.T., Baum N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
 RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
 RT "Cloning and characterization of a secreted frizzled-related protein
 RT that is expressed by the retinal pigment epithelium.";
 RL Hum. Mol. Genet. 8:575-583(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshitoki S., Carrinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gumatrine P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Soluble frizzled-related proteins (sFRPs) function as
 CC modulators of Wnt signaling through direct interaction with Wnts.
 CC They have a role in regulating cell growth and differentiation in
 CC specific cell types. sFRPs may be involved in determining the
 CC polarity of photoreceptor, and perhaps other, cells in the retina.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein

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CC (GPR) family.
CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AF117759; AAD25053.1; -; mRNA.
DR EMBL: BC032921; AAH32921.1; -; mRNA.
DR HSSP: OG1091; 110Y.
DR MGI: MGI:1860298; Strp5.
DR GO: GO:0005615; Cytoplasmic space; TAS.
DR InterPro: IPR000024; Fz domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00643; C34SC; 1.
DR SMART: SM00643; FRI; 1.
DR PROSITE: PS50038; Fz; 1.
DR PROSITE: PS50189; NTR; 1.
DR Developmental protein: Differentiation; Signal; Wnt signaling pathway.
KW SIGNAL
FT CHAIN 1 21 Potential.
FT DOMAIN 22 314 Secreted frizzled-related protein 5.
FT DOMAIN 45 162 Fz.
FT DISULFID 178 300 NTR.
FT DISULFID 50 113 By similarity.
FT DISULFID 60 106 By similarity.
FT DISULFID 97 132 By similarity.
FT DISULFID 121 159 By similarity.
FT DISULFID 125 149 By similarity.
FT DISULFID 178 250 By similarity.
FT DISULFID 181 252 By similarity.
FT DISULFID 195 300 By similarity.
FT CONFLICT 128 128 A -> V (in Ref. 2).
SQ SEQUENCE 314 AA; 35382 MW; 296847F56D1CAFD CRC64;

Query Match
Best Local Similarity 93.2%; Score 1613; DB 1; Length 314;
Matches 295; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 7 AGCVTAALALALGALHMAPARCEEDYDYGMAEPHGRSYKPPQCLDIPADLPCHTV 66
DB 4 AMSASTAALALALGALHGAPTRGQEDYDYGMAEPHGRSYKPPQCLDIPADLPCHTV 63
QY 67 GYKRMRLPVLHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIPCRS 126
DB 64 GYKRMRLPVLHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIPCRS 123
QY 127 LCEAVRAGCAPLMEAYGFPWPEMLHCHKEPPLDNDLCIAVQFGLHPTAPRVTKICACQEM 186
DB 124 LCEAVRAGCAPLMEAYGFPWPEMLHCHKEPPLDNDLCIAVQFGLHPTAPRVTKICACQEM 183
QY 187 EHSADGLMEQWSSDFVVMRIKEIKIENGDRKILGAQKKKLLKPGPKRDTKRLVLA 246
DB 184 EHSADGLMEQWSSDFVVMRIKEIKIENGDRKILGAQKKKLLKPGPKRDTKRLVLA 243
QY 247 MNGAGCAPCPOLDLGLSFLVMGRKVDGOLLMAVYRMDKKNKEMKFAVKMESVPCSLY 306
DB 244 MNGAGCAPCPOLDLGLSFLVMGRKVDGOLLMAVYRMDKKNKEMKFAVKMESVPCSLY 303
QY 307 YPFFYGAAEPH 317
DB 304 YPFFYGAAEPH 314

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB MG69423 protein.
GN Name=MG69423;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Embryo.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S.N., Krzywinski M.I., Skalske U., Smalloe D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Embryo.
RA Klein S., Gerhart D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC074661; AAH74661.1; -; mRNA.
DR GO: GO:0016020; Cytoplasm; IEA.
DR GO: GO:004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0007275; P:development; IEA.
DR GO: GO:0016055; P:receptor signaling pathway; IEA.
DR InterPro: IPR000024; Fz domain.
DR InterPro: IPR01134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00643; C34SC; 1.
DR SMART: SM00643; FRI; 1.
DR PROSITE: PS50038; Fz; 1.
DR PROSITE: PS50189; NTR; 1.
SQ SEQUENCE 315 AA; 36455 MW; 9DB8E912FB3A386 CRC64;

Query Match
Best Local Similarity 67.1%; Score 1160.5; DB 2; Length 315;
Matches 203; Conservative 47; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPARCEEDYDYGMAEPHGRSYKPPQCLDIPADLPCHTVGYKRMRLP 74
DB 13 SLILGLVMSA--BEYDYYWGQSDNFGNGFYRKQSCIDIPSDHLCHVGVKXKRLP 70
QY 75 NLLHESLAEVKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIPCSLCEAVRAG 134
DB 71 NLLDHEITPVEYKQQAASSWLPILAKRCHSDTVFLCSLPAPVCLDRPIPCSLCEAVRAG 130
QY 135 CAPLMEAYGFPWPEMLHCHKEPPLDNDLCIAVQFGLHPTAPRVTKICACQEMHSADGLM 194
DB 131 CAPVMEAYGFPWPEMLHCHKEPPLDNDLCIAVQFGLHPTAPRVTKICACQEMHSADGLM 190
QY 195 EOMCSDFVVMRIKEIKIENGDRKILGAQKKKLLKPGPKRDTKRLVLMKNGAGCAP 254
DB 191 VQLCASDFVLMRIKEIKIENGDRKILGAQKKKLLKPGPKRDTKRLVLMKNGAGCAP 250

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QY 255 CPOLDSLAGSFLWGRKVDGOLLMAVYRMDKKNKEMKFAVPMFSPCS 304
DB 251 CPQJNLSSGFLIMGRKVDNKLTLTAIYKMDKSKDMKAVANPMFSPCS 300

RESULT 5

Q8AWG4 XENLA PRELIMINARY; PRT; 315 AA.

AC Q8AWG4;
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Secured frizzled-related protein 5.
GN Name=FRP5;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22505169; PubMed=12617827; DOI=10.1016/S1567-133X(02)00023-6;
RA Pilcher K.E., Kriegl P.A.;
RT "Expression of the Wnt inhibitor, sFRP5, in the gut endoderm of
RT Xenopus.";
RL Gene Expr. Patterns 2:369-372(2002).
DR EMBL; AY164461; AAN87352.1; -; mRNA.
DR HSRP; O61091; 110Y.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016055; P:mtc receptor signaling pathway; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 315 AA; 36441 MW; 208E7706AC9ED431 CRC64;

Query Match 66.9%; Score 1157.5; DB 2; Length 315;
Best Local Similarity 69.7%; Pred. No. 3.2e-97;
Matches 202; Conservative 48; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPRCEBYDYWGQAEPL-HGRSYKRPQCLDIPADLPICHTVGYKRMRLP 74
DB 13 SYLLGLVLMSSA--EEDYYSWQSDNFPQGRFYTKQSCIDIPSDIHLCHNVGYKMRLLP 70
QY 75 NILHESLAEVQQAQSSWPLILAKRCHSDTOVFLCSLPAICLERIYPCRSICEVAVRAG 134
DB 71 NILDHTMEBYVQAQSSWVPLILAKRCHSDTOVFLCSLPAICLERIYPCRSICEVAVRDS 130
QY 135 CAPLMEAYGFPMPEMLHGHKFLPDLNDLCTAVFGHLPATAPRYTKCAQCEMEHSADGLM 194
DB 131 CAPWHESTGFPMPEMLHGHKFLPDLNDLCTAVFGHLPATAPRYTKCAQCEMEHSADGLM 190
QY 195 EQMGSSDFFVKKRIKIKIENGDRKILGAQKKKKLLKPPILRRKDKTKRLVLMKNGACGP 254
DB 191 VQLCASDFVLRMRIRKIKIENGDRKILGAQKKKKLLKPPILRRKDKTKRLVLMKNGACGP 250
QY 255 CPOLDSLAGSFLWGRKVDGOLLMAVYRMDKKNKEMKFAVPMFSPCS 304
DB 251 CPQJNLSSGFLIMGRKVDNKLTLTAIYKMDKSKDMKAVANPMFSPCS 300

RESULT 6
Q64003 XENLA PRELIMINARY; PRT; 315 AA.
AC Q64003;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DB LOC494659 protein.
GN Name=LOC494659;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen.
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carinini P., Scheetz T.E.,
RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan K.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman D.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalski S., Smalins D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX Klein S., Gerhard D.S.;
RL Submitted (Sep-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC082632; AAN82632.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016055; P:mtc receptor signaling pathway; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 315 AA; 36445 MW; 103E7BF4B957C035 CRC64;

Query Match 66.8%; Score 1155.5; DB 2; Length 315;
Best Local Similarity 69.7%; Pred. No. 4.8e-97;
Matches 202; Conservative 48; Mismatches 37; Indels 3; Gaps 2;

QY 16 ALLGALHMAPRCEBYDYWGQAEPL-HGRSYKRPQCLDIPADLPICHTVGYKRMRLP 74
DB 13 SYLLGLVLMSSA--EEDYYSWQSDNFPQGRFYTKQSCIDIPSDIHLCHNVGYKMRLLP 70
QY 75 NILHESLAEVQQAQSSWPLILAKRCHSDTOVFLCSLPAICLERIYPCRSICEVAVRAG 134
DB 71 NILDHTMEBYVQAQSSWVPLILAKRCHSDTOVFLCSLPAICLERIYPCRSICEVAVRDS 130

QY 135 CAPLMEAYGFWPMPWMLHCHKFPPLDNDLCIAVOGHLPTATPVPYTKICAOCEMEHSADGLM 194
 DB 131 CAPVMESSYGFWPMPWMLNCKFPPLDNDLCITVQFGSKQVQPPVTKICTQCEIEQSETR 190
 QY 195 EOMGSSDFVKKRIEIKIENGDRKLIQAOKKKKLLKQGPLKRXDTKLVLMKKGAGCP 254
 DB 191 VOLCSDPFLNRKRIEIKIENGDRKLIQAOKKKKLVKQGLKRRKFRKLVLYTKNAASCP 250
 QY 255 CPQDLSLGSFLVMGRKYDQGLLMAVYRWMDKKNKEMKFAVFMFSYPCS 304
 DB 251 CPQDLSLGSFLVMGRKYDQGLLMAVYRWMDKKNKEMKFAVFMFSYPCS 300

RESULT 7
 Q4SKX3 TESTNG PRELIMINARY; PRT; 321 AA.
 AC 04SKX3_

DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Chromosome 17 SCAF14563, whole genome shotgun sequence.
 DE (Fragment).
 CN ORFNames=GSTENG00016514001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 CX NCBI_Taxid=99863;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Maucel E., Bounau D., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Lheret S., Lucifalla G., Dossat C., Segurens B.,
 RA Daellva C., Salanoubat M., Levy M., Boudet N., Castellan S.,
 RA Anthouard V., Juhin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Catcolico L., Poulain J., De Berardinis V.,
 RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Landier E.S., Weissenbach J., Roest Crolious H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014563; CAP98709.1; -; Genomic_DNA.
 FT NON TER 321 321
 SQ SEQUENCE 321 AA; 36657 MW; 3060A2F9AD478156 CRC64;

Query Match 63.8%; Score 1104.5; DB 2; Length 321;
 Best Local Similarity 65.9%; Pred. No. 2.3e-92;
 Matches 201; Conservative 41; Mismatches 58; Indels 5; Gaps 2;

QY 7 AGGVTAAATLALGALHWAAPARCEEDYGYGQAEPLH-GRSYSKPQCLIDIPADLPCHT 65
 DB 20 AAGLSVFSLLILLITVSA----DEVDYYSWQSDNPNHGRFPYTKQPCQCDIVDRLCLN 75
 QY 66 VGYKMRLLPNLLHESLAEVKKQASWMLFLAKRCHSDTQVFLCSLPAFVCLDRIPYPCR 125
 DB 76 VGYKMRLLPNLLHESLAEVKKQASWMLFLAKRCHSDTQVFLCSLPAFVCLDRIPYPCR 135
 QY 126 SLCEAVRAGCAPLMEAYGFWPMPWMLHCHKFPPLDNDLCIAVOGHLPTATPVPYTKICAOCE 185
 DB 136 SLCEAVRAGCAPLMEAYGFWPMPWMLHCHKFPPLDNDLCIAVOGHLPTATPVPYTKICAOCE 195

QY 186 MEHSADGLMEOMGSSDFVKKRIEIKIENGDRKLIQAOKKKKLLKQGPLKRXDTKLV 245
 DB 196 NELRADNIMHEYCASDFLKKRIEIKIENGDRKLIQAOKKKKLVKQGLKRRKFRKLVLYTKNAASCP 250
 QY 246 HMKKGAGPCQDLSLGSFLVMGRKYDQGLLMAVYRWMDKKNKEMKFAVFMFSYPCS 305
 DB 256 YIKGANCPCQDLSLGSFLVMGRKYDQGLLMAVYRWMDKKNKEMKFAVFMFSYPCS 315
 QY 306 YYPEF 310
 DB 316 YHTVF 320

RESULT 8
 O6YNR8 BRARE
 ID O6YNR8 BRARE PRELIMINARY; PRT; 310 AA.
 AC O6YNR8_

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Secreted frizzled-related protein 1 (Secreted frizzled-related protein
 DE 5).
 CN Name=sfrp5; Synonyms=frpl;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX NCBI_Taxid=7955;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Shin U., Kim S.H., Yeo S.Y., Huh T.L.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umedin T.B., Toshimiki S., Carrinck P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krywinski M.I., Skalska U., Smallie D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Larvae;
 RG NIH MGC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050560; AAH11439.1; -; mRNA.
 DR EMBL; BC085455; AAH85455.1; -; mRNA.
 DR ZFIN; ZDB-GENE-011108-2; sfrp5.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0016055; P:ant receptor signaling pathway; IEA.
 DR InterPro; IPR00134; Netrin_C.
 DR InterPro; IPR01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR Pfam; SM00643; C345C; 1.
 DR SMART; SM00643; C345C; 1.

DR SMART; SM00063; FR1; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS0189; NTR; 1.
 SQ SEQUENCE 310 AA; 35393 MW; 77D3412C6CCCE8EA4 CRC64;
 Query Match 62.9%; Score 1089; DB 2; Length 310;
 Best Local Similarity 65.7%; Pred. No. 5.7e-91;
 Matches 197; Conservative 41; Mismatches 56; Indels 6; Gaps 2;
 QY 12 TAAATLLGALHAPARCEYDYGYGQAEPLH-GRSXRKPCQCLDIPADLPCHTGYGKR 70
 DB 15 TLALVLTSA-----SSAEYDYYSWQSDMFHSGRFAKQPCQVDIPADRLCTYNGYKK 69
 QY 71 MRLPNLLEHSLAEVAKQASWMLPLAKRCHSDTOYFLCSLFAVPCIDREIYPCRSICEA 130
 DB 70 MRLPNLDHETMEVAGQAGNSWPLAKRCHADTOYFLCSLFAVPCIDREIYPCRSICEA 129
 QY 131 VRAGCAPLMEAYGPPPEMLHCKHPLNDLCIAVOFGHLPATAPRYTKI CAOCMEHSA 190
 DB 130 VRDSCAPVMEYTGFPWPEMLQCEKFPIDNLCIPMOFSAGHATQTEVSKVCPDNEMLA 189
 QY 191 DGLMEQCSDFVYKRIKIKIENGDRKLI GAOKKKKLLKPGPLRKDKTKRLVLMKNG 250
 DB 190 DTMEHYCASDFALKMKIKKAKKEGDRKLI AOKKKKVLKMGILKDKDKLLTYIKNG 249
 QY 251 AGCPCPQLDSLAFVWGRKRVGOLLMAVYRWMDKKKEMKFAVFMESYPCSLYYPF 310
 DB 250 ANPCGQDLNLGSLFIMGRKVDQILLMSIHMDKSKSLKALIKYISQCPPTYHSVF 309
 RESULT 9
 SFRP1 HUMAN
 ID SFRP1 HUMAN STANDARD; PRT; 314 AA.
 AC 08N474; 000546; 014779;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Secreted frizzled-related protein 1 precursor (SFRP-1) (Frizzled-related protein 1) (FRP-1) (Secreted apoptosis-related protein 2) (SARP-2).
 GN Name=SFRP1; Synonyms=FRP, FRP1, SARP2;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 39-78.
 RC TISSUE=Embryonic lung fibroblast;
 RX MEDLINE=97338093; PubMed=9192640; DOI=10.1073/pnas.94.13.6770;
 RA Finch P.W., He X., Kelley M.J., Uren A., Schaudies R.P., Popescu N.C., Rudloff S., Aaronson S.A., Varnus H.E., Rubin J.S.; Popescu N.C., "Purification and molecular cloning of a secreted, frizzled-related antagonist of Wnt action.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:6770-6775 (1997).
 RL [2]
 RN NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
 RP TISSUE=Heart;
 RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
 RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M., Fitzpatrick P.A., Kleter M.C., Tomei L.D., Mahaney S.R.; "SARPs: a family of secreted apoptosis-related proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641 (1997).
 RL [3]
 RN NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.
 RP PubMed=9724099;
 RX Zhou Z., Wang J., Han X., Zhou J., Linder S.; "Up-regulation of human secreted frizzled homolog in apoptosis and its down-regulation in breast tumors.";
 RT Int. J. Cancer 78:95-99 (1998).
 RL [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schermer A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP PROTEIN SEQUENCE OF 32-314, DISULFIDE BONDS, MASS SPECTROMETRY, N-LINKED GLYCOSYLATION, AND MUTAGENESIS OF ASN-173 AND ASN-263.
 RX PubMed=11741940; DOI=10.1074/jbc.M108533200;
 RA Chong J.M., Ueren A., Rubin J.S., Speicher D.W.; "Disulfide bond assignments of secreted Frizzled-related protein-1 provide insights about Frizzled homology and netrin modules.";
 RT J. Biol. Chem. 277:5134-5144 (2002).
 RL [6]
 RN INTERACTIONS WITH WNT1, WNT2 AND FRZ6.
 RP PubMed=10347172; DOI=10.1074/jbc.274.23.16180;
 RX Raficio A., Gazit A., Pramila T., Finch P.W., Yaniv A., Aaronson S.A.; "Interaction of frizzled related protein (FRP) with Wnt ligands and the frizzled receptor suggests alternative mechanisms for FRP inhibition of Wnt signaling.";
 RT J. Biol. Chem. 274:16180-16187 (1999).
 RL [7]
 RN INDUCTION.
 RP PubMed=11932307; DOI=10.1210/jc.87.4.1729;
 RX Fukuhabara K., Kariya M., Kita M., Shine H., Kanamori T., Kosaka C., Orii A., Fujita J., Fujii S.; "Secreted frizzled related protein 1 is overexpressed in uterine leiomyomas, associated with a high estrogenic environment and unrelated to proliferative activity.";
 RT J. Clin. Endocrinol. Metab. 87:1729-1736 (2002).
 RL [8]
 RN FUNCTION: Soluble frizzled-related proteins (SFRPs) function as modulators of Wnt signaling through direct interaction with Wnts. They have a role in regulating cell growth and differentiation in specific cell types. SFRP1 decreases intracellular beta-catenin levels (By similarity). Has antiproliferative effects on vascular cells, in vitro and in vivo, and can induce, in vivo, an angiogenic response. In vascular cell cycle, delays the G1 phase and entry into the S phase (By similarity). In kidney development, inhibits tubule formation and bud growth in mechanophori (By similarity). Inhibits WNT1/WNT4-mediated TGF-dependent transcription.
 CC -1- SUBUNIT: Interacts with WNT1, WNT2 and FRZ6. Interacts with WNT4 and WNT8 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular matrix-associated. Released by heparin-binding.
 CC -1- TISSUE SPECIFICITY: Widely expressed. Absent from lung, liver and peripheral blood leukocytes. Highest levels in heart and fetal kidney. Also expressed in testis, ovary, fetal brain and lung, leiomyoma cells, myometrial cells and vascular smooth muscle cells. Expressed in foreskin fibroblasts and in keratinocytes.
 CC -1- INDUCTION: Down-regulated in colorectal and breast tumors. Up-regulated in uterine leiomyomas under high estrogenic conditions. Expression, in leiomyoma cells, also increased both under hypoxic and serum deprivation conditions.
 CC -1- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By similarity).
 CC -1- MASS SPECTROMETRY: MW=7266.4; METHOD=MALDI; RANGE=169-210;

```

CC NOTE=Isoform N-glycosylated on Asn-173 (Ref.5).
CC -1- MISCELLANEOUS: May have therapeutic use in cardiac surgery.
CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
CC (SFRP) family.
CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AF001900; AAB61576.1; -; mRNA.
CC EMBL, AF017987; AAB70793.1; -; mRNA.
CC EMBL, AF056087; AAC12877.1; -; mRNA.
CC EMBL, BC036503; AAB36503.1; -; mRNA.
CC HSSP, Q61091; 110Y.
CC Ensembl, ENSG00000104332; Homo sapiens.
CC HGNC, HGNC:10776; SFRP1.
CC MIM, 604156; -.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR001134; Netrin_C.
CC Pfam, PF01392; Fz; 1.
CC Pfam, PF01759; NTR; 1.
CC SMART, SM00643; C345C; 1.
CC SMART, SM00063; FRI; 1.
CC PROSITE, PS50038; FZ; 1.
CC PROSITE, PS50189; NTR; 1.
CC Developmental protein; Differentiation; Direct protein sequencing;
CC Glycoprotein; Signal; Wnt signaling pathway.
CC KW, SIGNAL 1 31
CC CHAIN 32 314
CC DOMAIN 53 169
CC FT 186 306
CC FT 173 173
CC FT CARBOHYD 58 121
CC FT DISULFID 68 114
CC FT DISULFID 105 140
CC FT DISULFID 129 166
CC FT DISULFID 133 157
CC FT DISULFID 186 236
CC FT DISULFID 189 258
CC FT DISULFID 203 306
CC FT MUTAGEN 173 173
CC FT MUTAGEN 263 263
CC FT CONFLICT 14 14
CC FT CONFLICT 174 174
CC FT CONFLICT 314 AA; 35386 MW; 29DD948706EB7143 CRC64;
SQ SEQUENCE

Query Match 53.4%; Score 924.5; DB 1; Length 314;
Best Local Similarity 56.6%; Pred. No. 6,3e-76;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;
1 MRAAAGAGGVRATALL--LGAALHMAAPARCEBYDYWGQAE--PLH-GRSYKRPQCVD 55
1 MGIGREGGRRGAALGVLTALGAALLAVGSASEYDYVSFGSDIGFYQSGFYTKPPQCV 60
1 IPADPLPLCHTVGKRRRLPMLLEHESLAEPYKQASMLPLAKRCHSDTQVFLCSLPAP 115
56 IPADPLPLCHTVGKRRRLPMLLEHESLAEPYKQASMLPLAKRCHSDTQVFLCSLPAP 115
61 IPADPLPLCHTVGKRRRLPMLLEHESLAEPYKQASMLPLAKRCHSDTQVFLCSLPAP 120
116 CLDRPIYPCRSGLCAVRAGCAPLMEAYGFPMPMLCHKRPFLNDNCIAVQGH-IPATY 174
121 CLDRPIYPCRSGLCAVRAGCAPLMEAYGFPMPMLCHKRPFLNDNCIAVQGH-IPATY 179
175 PAVTKCAQCEMEHSDGLMEOWCSSDFVYKRIKIKIENGDRKLIQAQKKKKLKPGE 234
180 PGTTVCPCPDNKLKSEALIEHLCASEFALRMKIKKIKKENGDKIV--PKKKKKPLKGP 237
235 LKRRDKRLVLYLHKNAGAGCPOLDLSLAGSFLYNGKRVGQQLIMAVYRDKKKNKMKRA 294
238 IKKKDKLKLVLTKNGADPCCHQLDNLSHFLIMGRKVSQYLLTALHKKDKKNKEKPN 297

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QY 295 VKMESYPCSLYYPF 310
DB 298 MKMKNHCECPRQSVF 313

RESULT 10
SFRP1_BOVIN STANDARD; PRT; 308 AA.
AC 09116;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE secreted frizzled-related protein 1 precursor (SFRP-1) (Frizzled in
DE aorta protein) (Fzr2 protein).
GN Name=SFRP1; Synonyms=FRZA;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=arteric endothelium;
RX MEDLINE=99316255; PubMed=10381896;
RA Duplaa C., Jaspard B., Moreau C., D'Amore P.A.;
RT "Identification and cloning of a secreted protein related to the
RT cysteine-rich domain of frizzled: evidence for a role in endothelial
RT cell growth control.";
RL Circ. Res. 84:1433-1445(1999).
CC -1- FUNCTION: Soluble frizzled-related proteins (SFRPs) function as
CC modulators of Wnt signaling through direct interaction with Wnts.
CC They have a role in regulating cell growth and differentiation in
CC specific cell types. SFRP1 decreases intracellular beta-catenin
CC levels (By similarity). Has antiproliferative effects on vascular
CC cells, in vitro and in vivo, and can induce, in vivo, an
CC angiogenic response. In vascular cell cycle, delays the G1 phase
CC and entry into the S phase (By similarity). In kidney development,
CC inhibits tubule formation and bud growth in metanephroi (By
CC similarity). Inhibits WNT1/WNT4-mediated TGF-dependent
CC transcription.
CC -1- SUBUNIT: Interacts with WNT1, WNT2, WNT4 and WNT8 and FRZD6 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular
CC matrix-associated. Released by heparin-binding.
CC -1- TISSUE SPECIFICITY: Highest levels in aortic endothelium, heart,
CC spleen and eye. Lower levels in lung, brain and kidney. Weak
CC expression in liver, skeletal muscle and the medial layer of the
CC aorta. In the cortical brain, localized to neurons and small blood
CC vessels. In the retina, localized to the inner and outer nuclear
CC layers with high expression in the neuronal cell bodies. In the
CC heart, restricted to myocytes. In lung, highest expression found
CC in the epithelium of terminal bronchioles. In kidney, localized to
CC the epithelium of collecting ducts of the medulla and, in spleen,
CC expression restricted to the red pulp in cells associated with the
CC sinuses.
CC -1- DOMAIN: The Fz domain is involved in binding with Wnt ligands (By
CC similarity).
CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
CC (SFRP) family.
CC -1- SIMILARITY: Contains 1 FZ (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, U85945; AAB67062.1; -; mRNA.
CC HSSP, Q61091; 110Y.
CC InterPro: IPR000024; Fz_domain.

```


RA Rattner A., Hsieh J.-C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
 RA Jenkins N.A., Nathans J.;
 RT "A family of secreted proteins contains homology to the cysteine-rich
 RT ligand-binding domain of frizzled receptors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kleener R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang Y., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Tothlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Lonnell N.A., Peters G.J., Abramson R.D., Millhy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 43-314.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354663; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikdel I., Oseto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Temaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
 RA Baldrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisai R.W.,
 RA Blake J.H., Bradt D., Brusic V., Chotcha C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Masahina T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempie C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [4]
 RN FUNCTION AS AN ANGIOGENIC FACTOR.
 RP PubMed=15306229; DOI=10.1016/j.cardiores.2004.05.006;
 RA Ezan J., Letour L., Barrandon L., Dufourcq P., Jaspard B., Moreau C.,
 RA Allieres C., Darot D., Couffignal T., Duplaa C.;
 RT "Frz/serp-1, a secreted antagonist of the Wnt-Frizzled pathway,
 RT controls vascular cell proliferation in vitro and in vivo.";
 RT Cardiovasc. Res. 63:731-738(2004).
 RN [5]
 RN DEVELOPMENTAL STAGE.
 RP PubMed=9739103; DOI=10.1016/S0925-4773(98)00072-0;

RA Leinleiter C., Bach A., Geesler M.;
 RT "Developmental expression patterns of mouse *serp* genes encoding
 RT members of the secreted frizzled related protein family.";
 RT Mech. Dev. 75:29-42(1998).
 RN [6]
 RN INTERACTION WITH WNT9, AND DEVELOPMENTAL STAGE.
 RP PubMed=10640709; DOI=10.1016/S0925-4773(99)00236-1;
 RA Jaspard B., Couffignal T., Dufourcq P., Moreau C., Duplaa C.;
 RT "Expression pattern of mouse *serp-1* and *wnt-8* gene during heart
 RT morphogenesis.";
 RT Mech. Dev. 90:263-267(2000).
 CC -1- FUNCTION: Soluble frizzled-related proteins (serps) function as
 CC modulators of Wnt signaling through direct interaction with Wnts.
 CC They have a role in regulating cell growth and differentiation in
 CC specific cell types. *serp1* decreases intracellular beta-catenin
 CC levels (By similarity). Has antiproliferative effects on vascular
 CC cells, in vitro and in vivo, and can induce, in vivo, an
 CC angiogenic response. In vascular cell cycle, delays the G1 phase
 CC and entry into the S phase. In kidney development, inhibits tubule
 CC formation and bud growth in metanephros (By similarity). Inhibits
 CC WNT1/WNT4-mediated TCF-dependent transcription (By similarity).
 CC -1- SUBUNIT: Interacts with WNT1, WNT2, WNT4 and
 CC FRZP5 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Cell membrane or extracellular
 CC matrix-associated. Released by heparin-binding (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in kidney and embryonic
 CC heart. Also highly expressed in the eye, where it is principally
 CC localized to the ciliary body and the lens epithelium. Weaker
 CC expression in heart, lung and brain. In the brain, is expressed
 CC exclusively in the choroid plexus.
 CC -1- DEVELOPMENTAL STAGE: In the developing kidney expressed at 13.5
 CC dpc in the periphery of the metanephros and surrounding the uretic
 CC and nephrogenic tubules. At 14.5 dpc, expression decreases in the
 CC outer cortical cells and becomes visible in the tubular parts of
 CC the nephron. From 15.5 dpc, highly expressed in the future loops
 CC of Henle. In the developing CNS, expression located to the future
 CC forebrain and hindbrain. At 8.0 dpc, expressed in the future
 CC forebrain and in the ventral portion of the presumptive hindbrain.
 CC At 8.5 dpc, expression is maintained in these tissues with a
 CC strong signal in rhombomere 4. Until 11.5 dpc, expression
 CC continues in the hindbrain with additional expression at 9.5 dpc
 CC and 10.5 dpc, in the nasal and ephranchial placodes. In the
 CC forebrain, initial expression is found in the telencephalon of the
 CC forebrain, and then strong expression in the telencephalic vesicle
 CC up to 15.5 dpc. Expression is then found in specific cell
 CC populations throughout the brain. In the developing eye,
 CC expression, by 10.5 dpc, is confined to ectodermal cells overlying
 CC the dorsal part of the optic cup. In later stages, expression
 CC limited to the lens fiber cells and the future pigmented retina.
 CC By 15.5 dpc, expression is confined to the anterior part of the
 CC lens. During limb development, barely expressed until later
 CC stages, when it is found in the distal part of the separating
 CC phalanges. In other developing structures, expressed in nasal
 CC placodes at 9.5 dpc, in medial nasal processes at E10.5 and then
 CC in the anterior portion of the invaginating olfactory epithelium.
 CC At 15.5 dpc, expressed on the basal side of the nasal epithelium.
 CC Also expressed in developing teeth, with the highest levels at
 CC 15.5 dpc and 16.5 dpc in the mesenchyme and the dental epithelium
 CC of the developing molars. As well, expressed in the ventral body
 CC wall, in the mesenchyme derived adrenal cortex, the cochlear
 CC epithelium and the branching epithelium of the salivary gland. In
 CC the developing heart, weakly expressed from 8.5 dpc in the tubular
 CC heart endocardium and myocardium. From 8.5 dpc to 12.5 dpc
 CC expressed in cardiomyocytes. At 9.5 dpc, expression found in the
 CC common ventricular and atrial chamber of the developing heart, in
 CC the aortic sac and in the sinus venosus. High expression found
 CC from 11.5 dpc-12.5 dpc, in the trabeculated wall of the
 CC ventricular chamber together with the wall of the atrial chamber.
 CC Expression also found in the muscular part of the interventricular
 CC septum. From 9.5 dpc-11.5 dpc expression in the visceral yolk sac
 CC confined to the inner lining endothelial cell layer. Expression
 CC in the developing heart decreases after 14.5 dpc.
 CC -1- DOMAIN: The F2 domain is involved in binding with Wnt ligands (By

```

CC similarity).
CC -1- SIMILARITY: Belongs to the secreted frizzled-related protein
CC (sfrp) family.
CC -1- SIMILARITY: Contains 1 Fz (frizzled) domain.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U88566; AAC53145.1; -; mRNA.
CC EMBL: BC024495; AAH24495.1; -; mRNA.
CC EMBL: AK081052; BAC39123.1; -; mRNA.
CC HSSP: OC1091; 11UY.
CC MGI: MGI:892014; Strpl.
CC GO: GO:0005615; C:extracellular space; TAS.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR001134; Netrin_C.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF01759; NTR; 1.
CC SMART: SM00643; C345C; 1.
CC SMART: SM00063; FRI; 1.
CC PROSITE: PS50038; FZ; 1.
CC PROSITE: PS50189; NTR; 1.
CC Developmental protein; Differentiation; Glycoprotein; Signal;
CC Wnt signaling pathway.
CC KMWnt signaling pathway.
CC FT SIGNL 1 31 Potential.
CC FT CHAIN 32 314 Secreted frizzled-related protein 1.
CC FT DOMAIN 53 169 FZ.
CC FT CARBOHYD 173 173 NTR.
CC FT DISULFID 58 121 N-linked (GlcNAc...) (By similarity).
CC FT DISULFID 68 121 By similarity.
CC FT DISULFID 105 140 By similarity.
CC FT DISULFID 129 166 By similarity.
CC FT DISULFID 133 157 By similarity.

Query Match 52.2%; Score 903; DB 1; Length 314;
Best Local Similarity 55.3%; Pred. No. 5; 9e-74; Mismatches 82; Indels 8; Gaps 5;
Matches 173; Conservative 50;

2 RAANAAGVYATALLLGLAHWPACREEDYDVGWQAE---PLHGRSYKSPQCLDIPA 58
5 KSRKRGGAAGVLLALAAAL-LAAGSASBYDVVSFOSDGSYGSRFTKPPQCDIIP 63
59 DLPLCHTVGYKRNRLPNLLEHESLAVYKQOASSMLPLAKRCHSDTQVFLCSLFAVVCID 118
64 DALCHNVGYKKNVLPVLEHETMAEVKQOASSWVPLNKNCHMGTVFLCSLFAVVCID 123
QY 119 RPIYPRGSLCEAVRAGCAPLMEAYGPPWPMMLCHKFPPLNDICIAVQFQH-LPATAFPV 177
DB 124 RPIYPRWLCBAVRDSCBPVMPQFPGFWPMLKCDKFP-BGDVCIAMTPPTTEAKPQO 182
QY 178 TKICACQEMHESADGLMEQCSSDFVYKRIKEIKIENGDRKLIQAOKKKKLLKPPPLK 237
DB 183 TTYVCPDNDLKESEALIEHLCASEFALRKIKKEYKKNQNDKIV--PKKKKPLKQPIK 240
QY 238 KDTKRLVLLHMKNGAGCPQOLDISLAGSFLVWGRKVDQQLLLMAVYRWDKKNKEMKFAVKF 297
DB 241 KELKALVLLFKNGADGCHQDNLNLSHNFILMGKRVKSQYLLTALHMKWDKKNKFAKPMKR 300
QY 298 MESYPCSLYYPFF 310
DB 301 MKNHCEPTFOSVF 313

```

```

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OX NCBI_Taxid=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210177; DOI=10.1016/j.mod.2004.03.003;
RA Esteve P., Lopez-Rios J., Bovolenta P.;
RT "SFRP1 is required for the proper establishment of the eye field in
RT the medaka fish."
RL Mech. dev. 121:687-701(2004).
DR EMBL: AY560904; AAS59408.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0007275; P:development; IEA.
DR GO: GO:0016055; P:wnt receptor signaling pathway; IEA.
DR InterPro: IPR000024; Fz domain.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01759; NTR; 1.
DR SMART: SM00643; C345C; 1.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS50038; FZ; 1.
DR PROSITE: PS50189; NTR; 1.
SQ SEQUENCE 306 AA; 34955 MW; 6D49B0FB9682C48C CRC64;

Query Match 49.2%; Score 851; DB 2; Length 306;
Best Local Similarity 52.7%; Pred. No. 3; 2e-69; Mismatches 74; Indels 26; Gaps 7;
Matches 164; Conservative 47;

11 RTAALALLGLAHWPACREEDYDVGWQAEPLH-GRSYKSPQCLDIPADLPLCHTVGYK 69
10 RWTQVILLAVTCGA-----SEYE-YTMAAGSYNGRGYGAQVQCDIPDRLCHTVGYT 64
QY 70 RKRPNLLEHESLAVYKQOASSMLPLAKRCHSDTQVFLCSLFAVVCIDRPIYPRSLICE 129
DB 65 QMLLPVLEHETMAEVKQOASSWVPLVHKNCHDKDQVFLCALFAVCEHPYPCWLCR 124
QY 130 AVRAGCAPLMEAYGPPWPMMLCHKFPPLNDICIAV-----QFGLPATAFPVYK 179
DB 125 TYRDCSPFLMEAFGPPWPMMLTCDKFPDQ-VCIATVQPNATEATPSSHSA----- 176
QY 180 ICAQCEMHESADGLMEQCSSDFVYKRIKEIKIENGDRKLIQAOKKKKLLKPPPLK 239
DB 177 -CPDCNIEIKNDAMLENICASEFALRKIKKEYKKNQNDKIV-LQRRKRVYKQNLKRD 234
QY 240 TKRVLVLLHMKNGAGCPQOLDISLAGSFLVWGRKVDQQLLLMAVYRWDKKNKEMKFAVKF 299
DB 235 LKRLTLVLLNGANGCPQOLENENQYLIMGRKVDKQPLTGIHMKWDKKNKFAKPMKR 294
QY 300 SYPCSLYYPFF 310
DB 295 NYKCPAFENVF 305

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RESULT 13
06GZKI_ORYLA PRELIMINARY; PRT; 306 AA.
AC 06GZKI;
DT 05-JUL-2004 (Tremblrel. 27, Created)

RESULT 14
SFRP1 CHICK STANDARD; PRT; 314 AA.
AC 09DEQ4;
DT 10-MAY-2005 (rel. 47, Created)
DT 10-MAY-2005 (rel. 47, Last sequence update)
DT 10-MAY-2005 (rel. 47, Last annotation update)
DE Secreted frizzled-related protein 1 precursor (sfrp-1) (Csfrp1).
GN Name=SFRP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.

Thu Mar 23 09:39:39 2006

DR PROSITE; PSS0038; F2; 1.
DR PROSITE; PSS0189; NTR; 1.
SQ SEQUENCE 311 AA; 35718 MW; 81C9E7153F445401 CRC64;

Query Match 48.4%; Score 836.5; DB 2; Length 311;
Best Local Similarity 55.1%; Pred. No. 7e-68;
Matches 158; Conservative 46; Mismatches 66; Indels 17; Gaps 7;

Qy	20	GALHMA	P	A	C	E	E	D	Y	Y	G	W	Q	---	A	E	P	L	H	G	R	S	Y	S	K	P	P	O	C	D	I	P	A	D	L	P	L	C	H	T	V	G	K	R	M	L	P	N	75										
Db	18	G	I	L	S	Q	V	P	-	Q	A	S	E	T	D	V	S	F	O	P	D	L	G	R	Q	Y	S	R	P	A	C	L	E	I	P	O	D	M	T	L	C	H	G	V	T	N	K	V	L	P	N	76							
Qy	76	L	I	E	H	E	S	I	A	E	V	K	Q	A	S	S	M	L	P	L	A	R	C	H	S	D	T	Q	V	F	L	C	S	L	F	A	P	V	C	L	D	R	P	I	P	C	R	S	L	C	E	A	V	R	A	G	135		
Db	77	L	I	D	S	E	T	M	A	E	V	K	Y	Q	A	S	S	M	V	P	L	S	K	C	H	P	S	T	Q	V	F	L	C	S	L	F	A	P	L	C	L	D	R	P	I	P	C	R	L	C	E	S	V	R	D	A	C	136	
Qy	136	A	P	L	M	E	A	Y	G	F	P	W	P	M	L	H	C	K	F	P	L	D	N	D	L	C	I	A	V	Q	G	H	L	P	-	A	T	A	P	-	-	V	T	K	I	C	A	Q	C	E	M	E	H	S	A	D	191		
Db	137	E	P	M	Q	Y	F	G	F	H	W	P	M	L	R	C	E	Q	Y	P	T	E	E	D	V	C	I	A	V	-	-	H	L	P	N	A	T	O	A	P	R	S	R	K	T	E	V	C	P	Q	C	D	S	E	I	K	A	D	193
Qy	192	G	M	E	Q	M	C	S	S	D	F	V	Y	K	M	I	K	E	I	K	I	E	N	G	D	R	K	L	I	G	A	Q	K	K	K	L	K	P	G	P	L	K	R	K	D	T	R	L	V	L	H	M	K	N	G	A	251		
Db	194	S	L	I	E	H	M	C	A	S	D	P	A	L	K	V	S	I	R	E	V	R	K	E	N	G	D	R	K	L	-	-	L	R	K	E	K	A	L	K	G	P	I	Q	K	D	M	A	E	L	V	L	K	N	G	A	251		
Qy	252	G	C	P	C	P	O	L	D	S	L	A	G	S	F	L	V	M	G	R	K	V	D	G	O	L	L	M	A	V	R	M	D	K	K	E	M	K	F	A	V	K	F	M	298														
Db	252	N	C	P	C	H	Q	L	D	L	K	G	F	V	L	G	P	R	A	K	A	Q	H	L	T	A	I	H	K	W	D	K	T	N	R	E	F	N	-	-	R	F	M	295															

Search completed: March 22, 2006, 22:42:16
Job time : 234 secs

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Query Match	16.1%;	Score 279;	DB 7;	Length 325;
Best Local Similarity	26.1%;	Pred. No. 1.9e-20;		
Matches	85;	Conservative	51;	Mismatches 106;
			Indels	84;
			Gaps	13;

RESULT 9
8-11-054-281-36
Sequence 36, Application US/11054281

PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324

Query Match	16.1%;	Score 278;	DB 7;	Length 591;
Best Local Similarity	36.7%;	Pred. No. 4.9e-20;		
Matches 65;	Conservative 23;	Mismatches 53;	Indels 36;	Gaps 7;

RESULT 10
US-11-054

US-11-054-281-1220

Db 110 ACRPMCEQARLRCAPIMEQNFQWPSDLCARLPTRNDFHALCMEAPEN--ATAGP 163

```

Db 4 PITPLKCDKLGYNLTSMNPLIGHTTQEEAGLELSQFYPYLLNQQCSPDILRFFLCSVYAPVC 63
OY 117 ----LDRIYPRSRSLCEAVRAGCAPLMEAYGFPWPMLHCHKRPPLNDLCI 163
Db 64 TADLPPEILLPCRSLSCEAAREGCEPLMEKFGFGWPEFLICDRPPVQNELCM 113

RESULT 7
US-11-184-005-7
; Sequence 7, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
; FILE REFERENCE: NIH133.1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-11-184-005-7

Query Match 16.5%, Score 285, DB 7, Length 319;
Best Local Similarity 27.8%; Pred. No. 4.5e-21;
Matches 76; Conservative 50; Mismatches 93; Indels 54; Gaps 11

OY 57 PADPLCHTVGYKKMKRLPNLLHSHSLAEVKKQASWMLBLAKRCHSDPTQVFLCSLPAPVC 116
Db 33 FVRILPMCKSMWNTKMPNHLHSHIOANAIIAIEQFEGILTTGCSODLLFLICAMYAPIC 92
OY 117 L----DRIYPRSRSLCEAVRAGCAPLMEAYGFPWPMLHCHKRP L-DNDLCIAVQF--- 167
Db 93 TIDQHEPIRKCKSVCEPARGACEPILIKYRHTWPESLACEPLPYVDGVCISPEAVITV 152
OY 168 -----GHLPATPAPVTYKICACQCEHSHADGLMEQMSDFFVKKRIKEI 211
Db 153 EQGTDSDPDPMSDNNNGCGSTA--GEHCKCKPKMASOKTYLKN--NNVYIRAKVKEV 207
OY 212 KIENGDRKLIGAKKKKLLKRGPLK-RKDTKRLVLHMKNAGAGCPGPDLSLAGSFLWMGR 270
Db 208 KVKCHDATAI--VERKETLKSSLVNIPKDTVTLV---TNSGCLCPOLVA-NBYIIMGY 260
OY 271 K-----VDGQV-----LIMAVYRMDKK 287
Db 261 EDKERTRLLLVSGSLAEKWRMDRLAKKVKRWQK 293

RESULT 8
US-11-184-005-2
; Sequence 2, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Wang, Shouwen
; APPLICANT: Hoang, Bang
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; TITLE OF INVENTION: GROWTH USING FRZB PROTEIN

```

Db 395 NFWKMKKMHCEPTFQSVF 412

RESULT 2

US-11-067-121-11
Sequence 2, Application US/11067121
Publication No. US20050261185A1
GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
PRIOR FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 295
TYPE: PRT
ORGANISM: Mus musculus
US-11-067-121-2

Query Match 35.9%; Score 620.5; DB 7; Length 295;
Best Local Similarity 44.1%; Pred. No. 6e-55;
Matches 127; Conservative 51; Mismatches 93; Indels 17; Gaps 7;

QY 13 ALALLLGLAHMARPACCEVDYIGWQAEPLHGRSYKRPQCLDIPADLPICHTVGYKRMRL 72
DB 6 ASILLFLVASHCCLSARGFLFG--OPDSYKRSNCKP-----IPANLQICHGIEYQNMRL 59
QY 73 LFNLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 129
DB 60 LFNLEHETMKEVLEBAGAMIPVMKQCHPDTKFLCSLPAPVCDDDDDETTOPCHSLCY 119
QY 130 AVRAGCAPLMEAYGFPWPEMLHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCEM 185
DB 120 QVKDCAPVMSAFGFPWPEMLECDRFPQDNDLCIPLASSDHLPLATEAP---KVCEACKN 176
QY 186 EHSADG-LMEQWSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLYL 244
DB 177 TKNEDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSKTIYKLVNGVSEBDLKSVL 236
QY 245 LHMKGAGCPCPOLDSLAFVLMGRKVDGOLLMAVYRMDKKNKEMK 292
DB 237 WLKDSLOCTCEBNDINAPVLMGQKOGELVITSVKRMQKQREPK 284

RESULT 3

US-11-067-121-11
Sequence 11, Application US/11067121
Publication No. US20050261185A1
GENERAL INFORMATION:
APPLICANT: Martijn, Cecile
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: THERAPEUTIC PROTEINS
FILE REFERENCE: 18909-002001
CURRENT APPLICATION NUMBER: US/11/067,121
PRIOR FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: US 60/576,445
PRIOR FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: SE 0400489-1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens

US-11-067-121-11

Query Match 35.5%; Score 614.5; DB 7; Length 295;
Best Local Similarity 43.9%; Pred. No. 2.4e-54;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 14 ALALLLGLAHMARPACCEVDYIGWQAEPLHGRSYKRPQCLDIPADLPICHTVGYKRMRL 73
DB 7 SILLFLVASHCCLSARGFLFG--OPDSYKRSNCKP-----IPANLQICHGIEYQNMRL 60
QY 74 FNLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 130
DB 61 FNLEHETMKEVLEBAGAMIPVMKQCHPDTKFLCSLPAPVCDDDDDETTOPCHSLCY 120
QY 131 VRAGCAPLMEAYGFPWPEMLHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCEM 186
DB 121 VKDCAPVMSAFGFPWPEMLECDRFPQDNDLCIPLASSDHLPLATEAP---KVCEACKN 177
QY 187 EHSADG-LMEQWSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLYL 245
DB 178 KNDNDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSKTIYKLVNGVSEBDLKSVL 237
QY 246 HMKNGAGCPCPOLDSLAFVLMGRKVDGOLLMAVYRMDKKNKEMK 292
DB 238 WLKDSLOCTCEBNDINAPVLMGQKOGELVITSVKRMQKQREPK 284

RESULT 4

US-11-051-720-1701
Sequence 1701, Application US/11051720
Publication No. US20060046257A1
GENERAL INFORMATION:
APPLICANT: Compugen Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
FILE REFERENCE: 1847.1002
CURRENT APPLICATION NUMBER: US/11/051,720
PRIOR FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1780
SEQ ID NO 1701
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-720-1701

Query Match 35.5%; Score 614.5; DB 7; Length 295;
Best Local Similarity 43.9%; Pred. No. 2.4e-54;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 14 ALALLLGLAHMARPACCEVDYIGWQAEPLHGRSYKRPQCLDIPADLPICHTVGYKRMRL 73
DB 7 SILLFLVASHCCLSARGFLFG--OPDSYKRSNCKP-----IPANLQICHGIEYQNMRL 60
QY 74 FNLEHESLAIEYKQOASWMLPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLSCE 130
DB 61 FNLEHETMKEVLEBAGAMIPVMKQCHPDTKFLCSLPAPVCDDDDDETTOPCHSLCY 120
QY 131 VRAGCAPLMEAYGFPWPEMLHCHKFPDLNDLCIAVOFGH--LPAT--APPVTKICAQCEM 186
DB 121 VKDCAPVMSAFGFPWPEMLECDRFPQDNDLCIPLASSDHLPLATEAP---KVCEACKN 177
QY 187 EHSADG-LMEQWSSDFVVKRIKIKIENGDRKLIQAQKKKLLKPGPLKROTRLYL 245
DB 178 KNDNDNDIMETLCKNDPALKIKVKEITYINRDTKILLETSKTIYKLVNGVSEBDLKSVL 237
QY 246 HMKNGAGCPCPOLDSLAFVLMGRKVDGOLLMAVYRMDKKNKEMK 292
DB 238 WLKDSLOCTCEBNDINAPVLMGQKOGELVITSVKRMQKQREPK 284

RESULT 5

US-11-051-720-1306
Sequence 1306, Application US/11051720

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PRIORITY APPLICATION NUMBER: 60/261,029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 585
TYPE: PRT
ORGANISM: Gallus gallus
US-11-054-281-92

Query Match      16.0%; Score 277.5; DB 7; Length 585;
Best Local Similarity 36.5%; Pred. No. 5.4e-20;
Matches 61; Conservative 22; Mismatches 57; Indels 27; Gaps 5;

QY      6 AAGGVRTRRALALLGLAHMMPARCEEEVDYYGMQAEPHIGRS--YSKPPQCLDIIPADLP LCH 62
        |||::|||
DB       4 AAGLVRAVAL-----C-----WLHEHCAGISSITIERGDGRCP EILPM 45

QY      63 CHTVGYRMRLEPNLLEHSIAEYVQOASSWMLPLAKRCHSDPTQVFSLTFAFVCLDR--- 119
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       46 CKDIGVMNTNPNLMGHENGRREALIQIHERFAPLYVEYGCHGLKRFELSLYAPMCTGEYST 105

QY      120 PIYCRSLCEAVRAGCAPLMEAYGFPPPEMLHCHKFLPDND---LCI 163
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       106 PIPACRVWCSEQARKCSPIMEQFNFKWPDSIDCSKLPIKNDPNYLICM 152


RESULT 13
US-11-184-005-8
Sequence 8, Application US/11184005
Publication No. US20050256052A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Malcolm JR.
APPLICANT: Hoang, Bang
APPLICANT: Wang, Shouwen
TITLE OF INVENTION: METHOD OF MODULATING TISSUE
TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
FILE REFERENCE: NIH133.ICP3
CURRENT APPLICATION NUMBER: US/11/184,005
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 10/028051
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 08/822333
PRIOR FILING DATE: 1997-03-20
PRIOR APPLICATION NUMBER: US 08/729,452
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 319
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-11-184-005-8

Query Match      16.0%; Score 276.5; DB 7; Length 319;
Best Local Similarity 25.8%; Pred. No. 3.3e-20;
Matches 84; Conservative 52; Mismatches 106; Indels 83; Gaps 13;

QY      7 AGGVRTALAILL--GALHMMPARCEEVDYYGMQAEPHIGRSYSKKPPQCLDIIPADLP LCH 64
        |||::|||
DB       12 AGLALAALCLRLVPGA--RAACE-----PRATPYCK 42

QY      65 TVGYKRMRLEPNLLEHSIAEYVQOASSWMLPLAKRCHSDPTQVFSLTFAFVCL---DRP 120
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       43 SLPPNMTKMRPHLHSHSQDANNILAIEQFEGLTGHCSPDLLFLPCAMVAPICTIDFGHEP 102

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Qy 121 IYPCSLCEAVAGCAPLMEAYGFPWPEMLHCHKPPL-DNDICIAVQGHLPATAPVTK 179
Db 103 IKPCSCVCEBAAQCGEPILIKYRHSHWPSBISLACEELPVYDYGVCISPE-----AIVTA 154
Qy 180 ICAQCEMHS---AGLMEQWC-----SSDFVVKMKIKIKIENGDRKLIG 222
Db 155 DGADPFPMDSNNGCRGASERCKCKPRATQKTYFRNNVYVIRAKVKEIKTKCHD--VTA 212
Qy 223 AOKKKKLLKPGPLKGRDTRKLVLMHKNAGACPCPOLDSLGSFLVMGRK-----VD 273
Db 213 VVEVEVEILKSSLV---NIPRDTVNLVYSSGCLCPPL-VNNEEYIIMGYEDEERSRLIVE 268
Qy 274 GOL-----LIMAVYRMDKKNEM 291
Db 269 GSIAEKMKDRLGKVKYRMDMKLRHL 293

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RESULT 14
US-11-184-005-4
; Sequence 4, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133, 1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-184-005-4

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Query Match 15.9%; Score 275; DB 7; Length 325;
Best Local Similarity 25.8%; Pred. No. 4.7e-20;
Matches 84; Conservative 52; Mismatches 106; Indels 84; Gaps 13;

```

```

Qy 7 AGGVTALALALL--GALHWAPARCEYDYGMQAEPLHGRSYSKRPOCLIDPADLPLCH 64
Db 14 AGLLALALCLLRVPGA---RAACE-----PVRIPLCK 44
Qy 65 TVGYKRMRLPNLLEHESLAEVQOASSWLPILAKRCHSDTQVFLCSLPAPVCL---DRP 120
Db 45 SLPMWMTKMPNHLHSTQANALIAIEQFGLLGTGHCSPDLFLCAMAYAPICITIDFQHEP 104
Qy 121 IYPCSLCEAVAGCAPLMEAYGFPWPEMLHCHKPPL-DNDICIAVQGHLPATAPVTK 179
Db 105 IKPCSCVCEBAAQCGEPILIKYRHSHWPSBISLACEELPVYDYGVCISPE-----AIVTA 156
Qy 180 ICAQCEMHS---ADGLMEQWC-----SSDFVVKMKIKIKIENGDRKLI 221
Db 157 DGADPFPMDSNNGCRGASERCKCKPRATQKTYFRNNVYVIRAKVKEIKTKCHD--VT 214
Qy 222 GAOKKKKLLKPGPLKGRDTRKLVLMHKNAGACPCPOLDSLGSFLVMGRK-----VD 272
Db 213 VVEVEVEILKSSLV---NIPRDTVNLVYSSGCLCPPL-VNNEEYIIMGYEDEERSRLIVE 268
Qy 274 GOL-----LIMAVYRMDKKNEM 291
Db 269 GSIAEKMKDRLGKVKYRMDMKLRHL 293

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RESULT 15
US-11-127-877-63
; Sequence 63, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spiltlaels, Koensraad F. F.
; APPLICANT: laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-63

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Query Match 15.8%; Score 273; DB 7; Length 585;
Best Local Similarity 39.0%; Pred. No. 1.5e-19;
Matches 53; Conservative 23; Mismatches 50; Indels 10; Gaps 5;

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Qy 48 SKRPOCLIDPADLPLCHTVGYKRMRLPNLLEHESLAEVQOASSWLPILAKRCHSDTQVFL 107
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Qy 108 LCSLPAPVCL---DRPIPCSLCEAVAGCAPLMEAYGFPWPEMLHCHKPPL-IDND--- 160
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Qy 161 LCIAVQGHLPATAPP 176
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Search completed: March 22, 2006, 22:47:15
Job time : 24 secs

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GenCore version 5.1.7
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OM protein - nucleic search, us-10-768-566-1

Run on: March 23, 2006, 06:52:56 ; Search time 5745 Seconds
(without alignments)
3136.532 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAAGCVRATATALLG.....MFSYPCSLTYPPFYGAABPH 317

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: gb_ov:*
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7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1730	100.0	1852	8 BC050435	BC050435 Homo sapi
2	1730	100.0	1984	6 BD217902	BD217902 Gene fam1
3	1730	100.0	1984	6 AX565716	AX565716 Sequence

4	1730	100.0	1984	6 AX597116	AX597116 Sequence
5	1730	100.0	1852	6 AX701369	AX701369 Sequence
6	1730	100.0	1984	6 AF017988	AF017988 Homo sapi
7	1730	100.0	1993	8 AF117758	AF117758 Homo sapi
8	1721	99.5	1719	6 C0720585	C0720585 Sequence
9	1682	97.8	1280	6 E44023	E44023 Novel human
10	1656	95.7	1728	4 AF117757	AF117757 Bos tauru
11	1617	93.5	1813	9 BC032921	BC032921 Mus muscu
12	1613	93.2	1186	9 AF117759	AF117759 Mus muscu
13	1571	67.7	210385	9 AC106128	AC106128 Rattus no
14	1162.5	67.2	163348	9 AC119236	AC119236 Mus muscu
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17	1157.5	66.9	3043	5 AY164461	AY164461 Xenopus 1
18	1155.5	66.8	2075	5 BC082632	BC082632 Xenopus 1
19	1106.5	64.0	146124	8 AL358938	AL358938 Human DNA
20	1089	62.9	1846	5 AY050560	AY050560 Danio rer
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23	977	56.5	1755	6 CS105981	CS105981 Sequence
24	924.5	53.4	945	11 AY891055	AY891055 Synthetic
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26	924.5	53.4	1308	6 BD217906	BD217906 Gene fam1
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31	924.5	53.4	4500	6 AR253209	AR253209 Sequence
32	917	53.0	942	6 AR361925	AR361925 Sequence
33	917	53.0	942	6 AX482568	AX482568 Sequence
34	916	53.0	1017	6 AR361926	AR361926 Sequence
35	916	52.9	2075	6 AR253206	AR253206 Sequence
36	916	52.9	2075	6 AR361924	AR361924 Sequence
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38	916	52.9	2075	6 AX482567	AX482567 Sequence
39	916	52.9	2075	6 AX565707	AX565707 Sequence
40	916	52.9	2075	6 AX597107	AX597107 Sequence
41	916	52.9	2075	6 AX701365	AX701365 Sequence
42	916	52.9	2075	8 AF001900	AF001900 Homo sapi
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ALIGNMENTS

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LOCUS	BC050435	MGC:54179 IMAGE:61894781	complete cda.		
DEFINITION	Homo sapiens secreted frizzled-related protein 5, mRNA (CDNA clone				
ACCESSION	BC050435				
VERSION	BC050435.1	GI:29791957			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg,R.L., Felngold,E.A., Grouse,L.H., Derge,J.G.,				
AUTHORS	1 (bases 1 to 1852)				
	Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D.,				
	Altshul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K.,				
	Hopkins,R.E., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,				
	Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,				
	Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L.,				
	Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,				
	Carinci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,				
	Abramson,R.D., Mulek,S.J., Bosak,S.A., McEwan,P.J.,				
	McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richard,S.,				
	Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huliyil,S.S.,				
	Villalon,D.K., Muzny,D.M., Sodergren,E.U., Lu,X., Gibbs,R.A.,				
	Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,				

Db 276 GCGCTGACATGGGCGCGCGCGCTGCGAGAGTACGACTACTATGCTGGCGAGCGCGAG 335
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Qy 141 A1aTyG1yPheProTrpProGlnuMetLeuH1eCybH1eLybPheProLeuAapAapAap 160
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LOCUS AX597116 Sequence 77 from Patent WO02090992.
DEFINITION AX597116
ACCESSION AX597116
VERSION AX597116.1 GI:28397671
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Andrews, P., Draper, J. and Walsh, J.
TITLE Screening method

JOURNAL Patent: WO 02090992-A 77 14-NOV-2002;
Axordia Limited (GB)
FEATURES
source Location/Qualifiers
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Pred. No.: 1,726-141 Length: 1984
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Db 276 GCGCTGACATGGGCGCGCGCGCGCGCGTGCAGAGCGCGCGCTGCGCTGCGAGCGAG 335
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DEFINITION      AX701369
ACCESSION      AX701369
VERSION      AX701369.1 GI:29537018
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Andrews, P., Walsh, J. and Gokhale, P.
AUTHORS      Method for modulating stem cell differentiation using stem loop rna
TITLE      Patent: WO 03012082-A 38 13-FEB-2003;
JOURNAL      Axordia Limited (GB)

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ORIGIN
Alignment Scores:
Pred. No.:      1,72e-141      Length:      1984
Score:      1730.00      Matches:      317
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      100.0%      Indels:      0
DB:      6      Gaps:      0

US-10-768-566-1 (1-317) x AX701369 (1-1984)
QY      1 MetArAlaAlaAlaAlaAlaGlyValArgThrAlaAlaLeuAlaLeuGly 20
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QY      21 AlaLeuHisTrpAlaProAlaArgCysGluGluTYrAspTYrTYrGlyTrpGlnAlaGlu 40
Db      276 GCGCTGCACCTGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 335
QY      41 ProLeuHisGlyArgSerTYrSerIysProProGlnCysLeuAspIleProAlaAspLeu 60
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Db      696 CTCTGCATGCCGTGTGATGAGTGGACAGCTGCCGCCGACCGGCTCTCAAGTCAAGATC 755
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QY      201 AspPheValValIysMetCArgIleIysGluIleIysIleGluAsnGlyAspArgIysLeu 220
Db      816 GACTTGTGTGCTCAAAATGCGCATCAAGAGATCAAGATGAGAAATGGGAGACCGAAGCTG 875
QY      221 IleGlyAlaGlnIlyIysIysIysLeuLeuIysProGlyProLeuIysArgIysAspThr 240
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QY      241 IysArgLeuValIleuHisMetIysAsnGlyAlaGlyCysProCysProGlnLeuAspSer 260
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RESULT 6
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LOCUS      Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA,
DEFINITION      complete cds.
ACCESSION      AF017988
VERSION      AF017988.1 GI:2415418
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 (bases 1 to 1984)
AUTHORS      Melkonyan, H.S., Chang, W.C., Shapiro, J.P., Mahadevappa, M.,
TITLE      Fitzpatrick, P.A., Kiefer, M.C., Tomei, L.D. and Umansky, S.R.
JOURNAL      SARPs: a family of secreted apoptosis-related proteins
PUBMED      Proc. Natl. Acad. Sci. U.S.A. 94 (25), 13636-13641 (1997)
9391078
2 (bases 1 to 1984)
REFERENCE      Melkonyan, H., Prochazka, V. and Umansky, S.R.
AUTHORS      Direct Substitution
TITLE      Submitted (11-AUG-1997) LXR Biotechnology, Inc., 1401 Marina Way
JOURNAL      South, Richmond, CA 94804, USA

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DEFINITION	Novel human gene analogous to secretory mouse protein sFRP-1.			
ACCESSION	E44023.1 GI:18625175			
VERSION	JP 2000106889-A/1.			
KEYWORDS	unidentified			
SOURCE	unclassified			
ORGANISM	unclassified.			
REFERENCE	1 (baee 1 to 1280)			
AUTHORS	Fu,A. and Zu,Y.			
TITLE	Novel human gene analogous to secretory mouse protein sFRP-1			
JOURNAL	Patent; JP 2000106889-A 1 18-APR-2000;			
	SMITHKLINE BEECHAM CORP			
COMMENT				
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	PD	18-APR-2000		
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		COTK14/47.		
	PC	C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, PC		
		C12Q1/02, C12Q1/68,		
	PC	G01N33/53, G01N33/531, G01N33/566, G01N33/577//C12P21/08, PC		
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Oy	21 AlaleuhlstrPaIaPrOlaIarGcYsaIgLuInuryRaPYrTYrGYITrdGlnaIacln 40			

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AUTHORS			
TITLE	Chang,J.T., Esnuli,N., Moore,K., Li,Y., Zhang,S., Chew,C., Goodman,B., Ratner,A., Moody,S., Stetten,G., Campochiaro,P.A. and Zack,D.J.		
JOURNAL	Cloning and characterization of a secreted frizzled-related protein that is expressed by the retinal pigment epithelium		
REFERENCE	Hum. Mol. Genet. (1999) In press		
AUTHORS	2 (bases 1 to 1186)		
TITLE	Chang,J.T., Esnuli,N., Campochiaro,P.A. and Zack,D.J.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (05-JAN-1999) Ophthalmology, JHMT, 809 Maumenee, 600 N. Wolfe St., Baltimore, MD 21287-9289, USA		
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QY	27	AlaAlaCysGluGluGlyTyrAspTyrGlyTyrGlnAlaGluProLeuHiGlyTyrSer	46
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QY	67	GlyTyrTyrValMetArgLeuProAsnLeuLeuGluHiGlySerLeuAlaGlyValTyr	86
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QY	87	GlnGlnAlaSerSerTyrLeuProLeuLeuAlaTyrArgCysHiSerTyrThrGlnVal	106
Db	491	CAGCAGGAGAGAGCTGGCTGCCTGCCTGGCGCCAGAGCGCTGCACCTACACACCCAGGTC	550
QY	107	PheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyrProCysArgSer	126
Db	551	TTCCTGTCTGCTTGTGCTGCTCCGCTGCCGTGGACCGACCATGTACCCCTGCGCGCTGG	610
QY	127	LeuCysGluAlaValArgAlaGlyCysValaProLeuMetGluAlaTyrGlyPheProTrp	146
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Db	671	CCCGAGATGCTGCATGGCACAAATTCCCCCTGGACACAGACTCTGTGCATCCGCGGCGAG	730

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LOCUS		Rattus norvegicus 1	BAC CH230-149H17 (Children's Hospital Oakland Research Institute) complete sequence.	
DEFINITION		AC106128		
ACCESSION		AC106128		
VERSION		AC106128.6	GI:1193855	
KEYWORDS		HNC		
SOURCE		Rattus norvegicus (Norway rat)		
ORGANISM		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.		
REFERENCE		1 (bases 1 to 210385)		
AUTHORS		Muzny,D,Marle, Metzker,M,Lee, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Albrooke,S., Amlin,A., Anguiano,D., Anyalabechi,V., Ayodeji,M., Bace,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buay,C., Burck,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceaar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carrillo,L., De Anda,C., Dedrich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C., Faller,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Georegegis,E., Geer,K., Gill,R., Grady,M., Guerra,T., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Jackson,B., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,C., Kwois,C., Kraft,C.L., Lebow,H., Levin,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu W., Liu,Y., London,P., Longacre,S., Lopez,X., Lorenzenewa,L., Louisseg,H., Lorado,R.J., Lu X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmood,M., Malloy,K., Mangum,A.,		

```

Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
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Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczka,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.

TITLE
Direct Submission
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 210385)
AUTHORS
Worley,K.C.
TITLE
Direct Submission
JOURNAL
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 210385)
AUTHORS
Rat Genome Sequencing Consortium.
TITLE
Direct Submission
JOURNAL
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 210385)
REFERENCE
Worley,K.C.
TITLE
Direct Submission
JOURNAL
Submitted (30-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 30, 2003 this sequence version replaced gi:30580782.
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
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LOCUS	AC119236/c	163348 bp	DNA linear ROD 01-OCT-2003
DEFINITION	Mus musculus chromosome 19, clone RP24-213B12, complete sequence.		
ACCESSION	AC119236		
VERSION	AC119236.8	GI:33285101	
KEYWORDS	HTG.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Schurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 163348)		
AUTHORS	Birtren,B., Nusbaum,C. and Lander,E.		
JOURNAL	Mus musculus chromosome 19, clone RP24-213B12		
REFERENCE	unpublished		
AUTHORS	2 (bases 1 to 163348)		
	Birtren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,		
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	Tophan,K., Travers,M., Travis,N., Trifillio,J., Vassiliev,H.,		

TITLE
DIRECT Submission
JOURNAL
Submitted (320-Apr-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
AUTHORS
Birtten,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barina,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouthgalter,B., Camaratia,J., Chang,Y., Choepel,Y., Collimore,A., Cook,A., Cooke,P., Corum,B., Deatellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,U., Horron,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Troh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meidrim,J., Menes,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., O'Neil,D., Oliver,J., Peterson,K., Punphanang,P., Pierre,N., Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viet,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
DIRECT Submission
JOURNAL
Submitted (02-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
AUTHORS
Birtten,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barina,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouthgalter,B., Camaratia,J., Chang,Y., Choepel,Y., Collimore,A., Cook,A., Cooke,P., Corum,B., Deatellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,U., Horron,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Troh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meidrim,J., Menes,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., O'Neil,D., Oliver,J., Peterson,K., Punphanang,P., Pierre,N., Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viet,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
DIRECT Submission
JOURNAL
Submitted (26-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE
AUTHORS
Birtten,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barina,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouthgalter,B., Camaratia,J., Chang,Y., Choepel,Y., Collimore,A., Cook,A., Cooke,P., Corum,B., Deatellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,U., Horron,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Troh,K., Liu,X., Lui,A., Mabbitt,R., Maclean,C., McDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meidrim,J., Menes,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., O'Neil,D., Oliver,J., Peterson,K., Punphanang,P., Pierre,N., Rachupka,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viet,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

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TITLE
JOURNAL
COMMENT
Myman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-OCT-2003) Whitehead Institute/MIT Center for Genome
Research, 330 Charles Street, Cambridge, MA 02141, USA
On Jul 26, 2003 this sequence version replaced gi:32401630.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
----- Project Information
Center project name: L25239
Center clone name: 213_B_12
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1 (bases 1 to 189196)
 REFERENCE
 AUTHORS Harrison, E.
 TITLE Direct Submision
 JOURNAL Submitted (07-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Jul 26, 2002 this sequence version replaced gi:21955486.
 COMMENT
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submision corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the


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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

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Searched: 4996997 segs, 333346308 residues
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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XX	Human secreted apoptosis related protein (SARP) 3 cDNA coding region.	
KW	Human; ss; gene; metabolic disorder;	
KW	Secreted Apoptosis-Related Proteins 3; SARP3; Obesity; overweight;	
KW	diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;	
KW	insulin sensitivity; food intake; body weight change; glucose tolerance;	
KW	hyperplastic growth; cell differentiation; programmed cell death;	
KW	apoptosis; hypertrophic growth; modulator; agonist; antagonist;	
KW	antigenase; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;	
KW	adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.	
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OS	Homo sapiens.	
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XX	US2003143610-A1.	

PD 31-JUL-2003.
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PF 08-JAN-2003; 2002US-0346523P.
PR (MILL-) MILLENNIUM PHARM INC.
PA Xu H;
PI WPI: 2003-635956/60.
DR P-PSDB; ADA38289.
XX
XX
PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
PT by assaying the ability of the compound to modulate a secreted Apoptosis-
PT Related Proteins 3 (SARF3) nucleic acid expression or polypeptide
PT activity.
XX
XX
PS Disclosure; SEQ ID NO 3; 35PP; English.
XX
CC The invention discloses a method for identifying a compound for treating
CC a metabolic disorder which comprises assaying the ability of the compound
CC to modulate secreted Apoptosis-Related Proteins 3 (SARF3) nucleic acid
CC expression or polypeptide activity. Also claimed are methods for
CC modulating SARF3 mediated metabolic activity, treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity and a pharmaceutical formulation for
CC treating metabolic disorders. The metabolic disorders comprise obesity,
CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
CC ability of the compound to modulate SARF3 nucleic acid expression or
CC polypeptide activity is determined by detecting a SARF3 activity of a
CC cell, or by detecting modulation of the level of beta-catenin, leptin or
CC insulin sensitivity, food intake, body weight change, glucose tolerance,
CC hyperplastic growth, cell differentiation, programmed cell death or
CC hypertrophic growth. Modulating SARF3 mediated metabolic activity
CC comprises contacting a cell or tissue expressing the SARF3 with a SARF3
CC modulator. The compound or modulator comprises a small molecule SARF3
CC agonist or antagonist or inverse agonist, anti-SARF3 antibody, antisense
CC SARF3 molecule or ribozyme. The SARF3 mediated metabolic activity
CC comprises the ability to modulate lipid, glucose or insulin metabolism,
CC adipocyte growth, the differentiation of adipose cell progenitors into
CC adipocytes or programmed cell death. Treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity comprises administering a SARF3
CC modulator. The compound is an oligonucleotide encoding an antisense or
CC ribozyme molecule that targets SARF3 transcripts and inhibits translation
CC or an oligonucleotide that forms a triple helix with the promoter of the
CC SARF3 gene and inhibits transcription. The sequence presented is the
CC human SARF3 cDNA coding region.
XX
SQ Sequence 954 BP; 171 A; 313 C; 308 G; 162 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,41e-163 Length: 954
Score: 1730.00 Matches: 317
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0
US-10-768-566-1 (1-317) x ADA38290 (1-954)
QY 1 MetATGAlaAlaAlaAlaAlaGlyValArgThraAlaAlaLeuAlaLeuLeuGly 20
DB 1 ATGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 60
QY 21 AlaLeuHisTTrAlaProAlaArgCysGluGluTTrAspTTrTyrGlyTTrGlnAlaGlu 40
DB 61 GGGCTGCACTGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 120
QY 41 ProLeuHisGlyArgSerTyrSerLeuProProGlnCysLeuAspTrLeuProAlaAspTr 60
DB 121 CGGTCGACAGGGCGGGCTCTACTTCGACAGCGCGGCAAGTGGCTTGACATCCCTGCGACCTG 180

QY 61 ProLeuCysHisTTrValGlyTTrIleArgMetAlaGluProAsnLeuLeuGluHisGlu 80
DB 181 CGGCTCTGCGACACGGTGGGCTTACAGAGCGCATGCGGCTGCCAACCTCTGGAGACAG 240
QY 81 SerLeuAlaGluValIleGlnGlnAlaSerSerTTrPheLeuProLeuLeuAlaIleArgCys 100
DB 241 AGCCTGGCGGAGTAG 300
QY 101 HisSerAspTTrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgPro 120
DB 301 CACTGGAGATACGACAGTCTTCTGTCGCTCGCTTCTTGCGCCCTGTGTCGACCGGCC 360
QY 121 IleTyrProCysArgSerLeuCysGlnAlaValAlaGlnAlaGlyCysAlaProLeuMetGlu 140
DB 361 ATCTACCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 420
QY 141 AlaTyrGlyPheProTTrProGluMetLeuHisCysHisIlePhePheProLeuAspAsnAsp 160
DB 421 GCGTACGGGCTTCCCTGGCCTGAGATGCTGCATGCCACAGTTCCCTGGACACAGAC 480
QY 161 LeuCysIleAlaValAlaGlnPheGlyHisIleProAlaTTrAlaProProValTTrHisIle 180
DB 481 CTCTGCACTGCGGTGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCA 540
QY 181 CysAlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluMetCysSerSer 200
DB 541 TCGGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 201 AspPheValValIleMetAlaGlyIleIleGluIleIleValIleGluAlaAspArgIleIle 220
DB 601 GACTTGTGTGTCAAATGCGCATCAAGAGATCAAGATCAAGATCAAGATCAAGATCAAG 660
QY 221 IleGlyAlaGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 720
DB 661 ATTGAAGCCCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 780
QY 241 IlyArgLeuValIleHisMetIleIleIleIleIleIleIleIleIleIleIleIleIle 260
DB 721 AGCGGCTGGTGTCTGCATGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 LeuAlaGlySerPheLeuValMetGlyIleIleIleIleIleIleIleIleIleIleIle 280
DB 781 CTGGGGGCGAGCTTCTGCTCAATGGCGCGCAAGAGATGAGACAGTCTGCTCAATGG 840
QY 281 ValTyrArgTTrAspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 300
DB 841 GTCTACCGCTGGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 900
QY 301 TyrProCysSerLeuTTrTTrProPhePheTTrGlyAlaAlaGluProHis 317
DB 901 TACCCCTGCTCTCTACTACCTTCTTCTTACCGGGCGGAGAGAGAGAGAGAGAG 954
RESULT 2
ADA38288
ID ADA38288 strand; cDNA, 1905 BP.
AC
AC ADA38288;
XX
DT 20-NOV-2003 (first entry)
XX
XX Human secreted apoptosis related protein (SARF3) 3 cDNA.
DE Human; ss; gene; metabolic disorder;
XX Secreted Apoptosis-Related Proteins 3; SARF3; obesity; overweight;
KW diabetes; insulin resistance; cachexia; anorexia; beta-catenin; leptin;
KW insulin sensitivity; food intake; body weight change; glucose tolerance;
KW hyperplastic growth; cell differentiation; programmed cell death;
KW apoptosis; hypertrophic growth; modulator; agonist; antagonist;
KW antisense; ribozyme; lipid; glucose; insulin; adipocyte; differentiation;
KW adipose cell; adipocyte; anorectic; antidiabetic; immunomodulator.
XX Homo sapiens.
OS

The invention relates to modulating the differentiation of an embryonic stem cell, comprising: (a) providing a culture of embryonic stem cells; (b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cell; (c) forming a culture comprising embryonic stem cells and the ligand; and (d) growing the cell culture. Also included are: (1) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) any of 9 fully defined Mnt nucleic acid sequences; (ii) a nucleic acid molecule that hybridises to the nucleic acid in (i), and which encodes a ligand capable of modulating embryonic stem cell differentiation, or capable of binding a Mnt receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the cell; (2) Inhibiting the maintenance and/or differentiation of the embryonic stem cell; (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing at least one polypeptide or its active fragment, that are inhibitors of the Mnt signalling pathway; (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; or (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encoding a Mnt inhibitory polypeptide; (ii) a molecule which hybridises to the molecule of (i) and encodes a polypeptide capable of inhibiting Mnt signalling; and (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; and (4) A cell, therapeutic cell or cell culture obtainable by any of the methods cited above. The therapeutic cell of the present invention is useful in the treatment of an animal, preferably a human, comprising administering a cell composition comprising embryonic stem cells which have been induced to differentiate into at least one cell-type. The cell is also useful for the manufacture of a composition for use in treatment of diseases such as Parkinson's disease, Huntington's disease, motor neuron disease, heart disease, diabetes, liver disease (e.g. cirrhosis), renal disease and AIDS (acquired immunodeficiency syndrome). The present sequence is encodes a Mnt or Notch pathway protein (i.e. a ligand for the method of the invention)

Sequence 1984 BP; 353 A; 634 C; 627 G; 370 T; 0 U; 0 Other;

US-10-768-566-1 (1-317) x ABX75334 (1-1984)

QY I Mckrfgalaaalaaalaaaglygdyvalaagfmrhlaalalaaleuleuleugly 20
Db 216 ATGCGGCGCGCGCGCGCGCGCGCGGAGCGGACGCGCGCTGCGCTGCTGCGG 275
QY 21 Alaleuhistrpalaapoolaaagcybgjlugluryaaapryttrygltipdnalaglu 40

Db	276	GGCGTGCAC	TGGGGGGCGCGCGCGCTGGAGGAGTACGACTACTATGAGCTGGCAGCGGAG	335
QY	41	ProLeu	HiSGIYAqSerTYrSerLYeProGInCYbLeuAaP11eProAlAspLeu	60
Db	336	CCGGCTGCAC	GGCGCGCGCTCTACTCCACACCGCGCGAGCGCTTGGACATCCCTGGCCGACTG	395
QY	61	ProLeuCYbHiS	TRPValAGIYTYrLYeARMeKrgLeuProAaLeuLeuGluHiSGlu	80
Db	396	CCGGCTTCGCAC	ACAGGGGGCTACAGAGGACATGGCGCTGCCAACCTTGCTGGACACAGAG	455
QY	81	SeLeu	AGIValLYySGInGlnAlAsSerSerTRPLeuProLeuLeuAlLYyAsrCYs	100
Db	456	AGCGTGGCGGAA	GGTGAAGACAGCAGCAGCGAGCGAGCTGGCGGCTGGCTGGCCAAAGCGCTGC	515
QY	101	HiSerAsp	TRHrgInValPheLeuCYeSerLeuPheAlaProValCYbLeuAspArgPro	120
Db	516	CACCTGGATAC	GGAGGCTTCTCTGTGCTGTGCTCTTTCGCGCGCGCTGTCTTGACCGGCGCC	575
QY	121	ILeTYrProCYbAs	GSerLeuCYeGlnAlaValArgAlaGlyCYbAlaProLeuMeGlu	140
Db	576	ATCTACCCGCT	CGCGCTGGCTGTGGAGGCGGTGGCGCGCGCTGGCGCGCTCATGGAG	635
QY	141	AlaTYrGlyPhe	ProTRPProGluMeLeuHiSCYbHiSLySPheProLeuAspAsnAsp	160
Db	636	GCCTACGGCTT	CCCCCTGGCGCTGAGATCTGTGCACATCCACAAATTCGCCCTTGACAAACAGAC	695
QY	161	LeuCYbAlIeAla	ValAGInPheGlyHiSLeuProAlaThzAlaProProValThyLYsAlIe	180
Db	696	CTCTGCACAT	CGCGGTGCAGTTCTGGGCGACCTGCCCGCCACCGGCGCTCCAGTACCAAGATTC	755
QY	181	CysAlaGInCYb	GluMeGluHiSeraAlAspGlyLeuMeGluGlnMeCYeSerSer	200
Db	756	TGGCGCCAC	GTGTGAGATGAGACACAGTGTACGGCTCATGAGACGATGTGTCTCCAGT	815
QY	201	AspPheValIa	LYbMeTargIaLYeGluIleLYsAlIeGluAaNGlyAspArgLYbLeu	220
Db	816	GACTTTGGTG	CAAAATGCGCATCAAGAGATCAAGATGAGATGGAGACCGGAAAGCTG	875
QY	221	ILeGlyAlaGIn	LYbLYeLYeLeuLeuLYsProGlyProLeuLYsArgLYeAspThr	240
Db	876	ATTGGAGCC	CCAGAAAAAGAAAGACTGTCTCAAGCGCGGCGCCCTTGAAAGCGAAGACAC	935
QY	241	LYsArgLeuVal	LeuHiSMeLYyAsnAGIYAlaGlyCYbProCYbProGInLeuAspSer	260
Db	936	AAGCGCGCT	GGTGTGCACATGAAGATGGCGCGGCTGCGCTCCACACACTGGAACGC	995
QY	261	LeuAlaGlySer	PheLeuValMeGlyAYArgLYbValAspGlyGInLeuLeuMeTala	280
Db	996	CTGGCGGGC	ACACTTCCTGGTGTATGGCGCGCAAAATGAGATGAGACGTGCTGCTATGGCC	1055
QY	281	ValTYrArgT	TRPAspLYbLYeAsnLYeGluMeLYsPheAlaValLYsPheMePheSer	300
Db	1056	GTCTACCGCT	TGGACAAAGAAATGAGAGATGAAAGTTTGCACTCAATTCATGTCTTCC	1115
QY	301	TYrProCYbSer	LeuTYrTYrProPhePheTYrGlyAlaAlaGluProHiS	317
Db	1116	TACCCCTGCT	CCCTCTACTACCTTTCTTCTACACGGGCGGAGAGGCCAC	1166

RESULT 7	
AAD52563	
ID	AAD52563 standard; DNA; 1984 BP.
XX	
XX	
AC	AAD52563;
XX	
DT	02-MAY-2003 (first entry)
XX	
DE	SARP 3 DNA.
KW	Drug screening; toxicology assay; signalling pathway; SARP 3; gene; ds
XX	
OS	Unidentified.
XX	
PN	WO200290992-A2.

Claim 4; Page 6; 28pp; English.

This sequence encodes the human ATG-1709 protein of the invention. ATG-1709 is related to human secreted lipands for 7-transmembrane receptor/oxorexin and similar to murine sFRP-1. ATG-1709 polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the ATG-1709 gene using probes containing the ATG-1709 nucleotide sequence, and can diagnose diseases associated with ATG-1709

QY	175	roproValThrIlysleCYaAlaGlnCybGluMetGluHisSerAlaAspGlyLeuMet	194
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	294		313
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	297		316</

Search completed: March 23, 2006, 07:03:31
Job time : 698 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 06:59:31 ; Search time 4508 Seconds
(without alignments)
3290.041 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGAGVTRALALLLG.....MFSYPSLHYPPFYGAEPH 317

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=xlh
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-DB=EST-QFMT=fastap -SUFFX=p2n.rst -MTNMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs804
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-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_esc2:*
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4: gb_hic:*
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8: gb_esc7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1726	92.8	1819	4	CR596705 full-length
2	1421	89.1	875	10	AY410883
3	1386.5	80.1	1039	1	AL538532
4	1382	79.9	873	10	AY410884
5	1361.5	78.7	799	10	AY410885
6	1335	77.2	819	7	CJ025307
7	1102	63.7	635	7	CK626659

8	1099	63.5	934	5	BX715714	BX715714
9	1096	63.4	934	5	BX719991	BX719991
10	1079.5	62.4	1026	5	B0879095	B0879095
11	986	57.0	592	7	BP329572	BP329572
12	959	55.4	566	7	CP982574	CP982574
13	956	55.3	611	6	CD673335	CD673335
14	945	54.6	606	3	BP329610	BP329610
15	910	52.6	957	6	CD518814	CD518814
16	891	51.5	664	5	BY741671	BY741671
17	888	51.3	2704	4	AK088668	AK088668
18	871	50.3	2298	4	AK081052	AK081052
19	860	49.7	1141	8	DN664190	DN664190
20	827	47.8	738	5	BQ771388	BQ771388
21	814	47.1	730	11	CR806571	CR806571
22	808	46.7	562	6	CB609383	CB609383
23	794.5	45.9	610	3	BM490250	BM490250
24	789	45.6	835	6	CF152416	CF152416
25	786.5	45.5	779	6	CB247875	CB247875
26	782.5	45.2	1190	8	DN684942	DN684942
27	751	43.4	441	3	BM716341	BM716341
28	750.5	43.4	713	6	CB525580	CB525580
29	737	42.6	662	2	BB647191	BB647191
30	728	42.1	458	3	BM694123	BM694123
31	723.5	41.8	748	6	CB247054	CB247054
32	716.5	41.4	1330	8	DN684943	DN684943
33	715	41.3	516	10	CG646528	CG646528
34	714	41.3	530	6	CB782544	CB782544
35	713	41.2	709	5	BM847760	BM847760
36	707	40.9	532	1	AM765850	AM765850
37	706	40.8	1011	5	B0196604	B0196604
38	685	39.6	685	6	CF727313	CF727313
39	678.5	39.2	1291	6	CD518463	CD518463
40	673.5	38.9	647	1	AW957689	AW957689
41	657	38.0	664	7	CK686080	CK686080
42	653	37.7	516	5	BX521125	BX521125
43	649	37.5	824	8	CK337082	CK337082
44	647.5	37.4	846	8	CK401961	CK401961
45	646	37.3	1239	8	DN677708	DN677708

ALIGNMENTS

RESULT 1	CR596705	1819 bp	mRNA	linear	HTC 17-APR-2005
LOCUS	CR596705				
DEFINITION	Full-length cDNA clone CS0DF024YR06 of Fetal brain of Homo sapiens (human).				
ACCESSION	CR596705.1	GI:50477512			
VERSION	CR596705.1	GI:50477512			
KEYWORDS	HTC; cNSLT cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Li W.B., Gruber C., Jessee J. and Polayes D. Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 1819)				
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/InvitrogenCorporation1600				
REFERENCE	2 (bases 1 to 1819)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				

Db 123 TACAAAGCGATGCGGCTGCCCACTGTGAGACAGAGAGCTGGCCGAGTGAAGCAG 182
 Qy 88 GlnAlaSerSerTripleuProleuAlaLysArgCysHisSerAspThrGlnValPhe 107
 Db 183 CAGGCGAGAGAGCTGGCTGGCCGCTGCTGGCCAGCGCTGGCACTCGGATACGAGGTTTC 242
 Qy 108 LeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyProCysArgSerLeu 127
 Db 243 CTGTGCTGCTCTTTGCGCCCGCTGTCTGACCGGCCCATCTACCCGTGGCTGCTG 302
 Qy 128 CysGlnAlaValAlaArgAlaGlyCysAlaProleuMetGlnAlaTyArgIlePheProTriPro 147
 Db 303 TCGAGAGCGGTGGCGCCCGCTGGCGCGCTGCTCATGAGAGCCCTACCGCTTCCTGGCCCT 362
 Qy 148 GluMetLeuHisCysHisIlePhePheProleuAspAsnAspLeuCysIleAlaValGlnPhe 167
 Db 363 GAGATGCTGCACNN 422
 Qy 168 GlyHisLeuProAlaThrAlaProProValThrLysIleCysAlaGlnCysGluMetGlu 187
 Db 423 NNN 482
 Qy 188 HisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPheValIleLysMetArg 207
 Db 483 CACAGTGTGACGCGCTCATGAGCAGATGTGCTCCAGTGAATTTGTGCTCAAAATGCGC 542
 Qy 208 IleLysGlnIleLysIleGluGlnArgLysAspArgLysLeuIleGlyAlaGlnLysLysLys 227
 Db 543 ATCAAGAGATCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 602
 Qy 228 LysLeuLeuLysProGlyProleuLysArgLysAspThrLysArgLeuValLeuHisMet 247
 Db 603 AACGCTCTCAAGCGCGGCCCCCTGGAAGCCGAGAGACCAAGGCGCTGCTGCTGCAATG 662
 Qy 248 LysAsnGlyAlaGlyCysProCysProGlnLeuAspSerIleuAlaGlySerPheLeuVal 267
 Db 663 AAGAAATGGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 722
 Qy 268 MetGlyArgLysValAspGlyGlnLeuLeuLeuMetAlaValThrArgTrpAspLysLys 287
 Db 723 ATGGGCGGCAAAATGATGAGACAGCTGCTCATGCGCTGCTGCTGCTGCTGCTGCTGCTG 782
 Qy 288 AsnLysGluMetLysPheAlaValLysPheMetPheSerTyProCysSerLeuTyTrp 307
 Db 783 AATAGAGATGAATTTGTCAGTCAATTCATTTCTTCTACCCCTGCTCCTTACTAC 842
 Qy 308 ProPhePheTyGlyAlaAlaGluProHis 317
 Db 843 CTTTCTTCTGACGGGCGGCGAGCCCCAC 872
 RESULT 3
 AL538532 1039 bp mRNA linear EST 24-MAR-2004
 LOCUS AL538532 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS050F024IP06 5-PRIME, mRNA sequence.
 ACCESSION AL538532 GI:45714242
 VERSION AL538532.3
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 1039)
 REFERENCE
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:11261122.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5245.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna/CS050F024IP0601&c=5245.r.
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 1. 1039
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="CS050F024IP06"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_id="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 3,44e-130 Length: 1039
 Score: 1386.50 Matches: 277
 Percent Similarity: 95.84 Conservative: 0
 Best Local Similarity: 95.84 Mismatches: 10
 Query Match: 80.18 Indels: 7
 DB: 1 Gaps: 0
 US-10-768-566-1 (1-317) x AL538532 (1-1039)

Qy 1 MetArgAlaAlaAlaAlaAlaGlyCysValArgThrAlaAlaLeuLeuLeuGly 20
 Db 121 ATGCGGGCGGCG 180
 Qy 21 AlaLeuHisTrpAlaProAlaArgCysGlu-GluTyAspTyTrpGlyAlaAlaGly 40
 Db 181 GCGCTGCACTGGGCG 240
 Qy 40 UProleuHisGlyArgSerTySerLysProProGlnCysLeuAspIleProAlaAspLe 60
 Db 241 GCCGCTGACGCGCGCTCTACTCAAGCCCGGAGGCTTGACATCTCCCTGCGCGAGCT 300
 Qy 60 UProleuCysHisThrValGlyTyTrpLysArgMetArg-LeuProAsnLeuLeuGlnHisG 80
 Db 301 GCCGCTGCGCACAGGATGGGCTACAGCGATGGAGCTGCCCACTGCTGAGAGCAG 360
 Qy 80 LysLeuAlaGlyValLysGlnGlnAlaSerSerTripleuProleuAlaLysArgC 100
 Db 361 AGAGCTGGCCGAAATGAG 420
 Qy 100 YHisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgP 120
 Db 421 GCCACTCGGATACGAGAGCTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Qy 120 TollyTyProCysArgSerLeuCysGlnAlaValAlaArgAlaGlyCysAlaProleuMetC 140
 Db 481 CCATCTACCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Qy 140 LysAlaTyGlyPheProTriProGluMetLeuHisCysHisLysAspPheProleuAspAna 160
 Db 541 AGGCGCTACGCGCTTCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Qy 160 AspLeuCysIleAlaValGlnPheGlyHisLeuProAlaThrAlaProValThrLysI 180
 Db 601 ACCTTGATGACGCGTGGAGTTGGGCACTGGCCGCGCCAGCTCCTCAATGACCAAGA 660
 Qy 180 LysCysAlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSer 200
 Db 661 TCTGGCGCCAGTGTGATGAGAGCAGATGTGAGCGGCTCATGAGAGAGATGTGCTCA 720

Db	1	CGCTGCAGAGGAGTACGACTACTATGCTGTGCAGGCGCAGCGCTGCACGGCCGCTCTTAC	60
OY	48	SetiyspProPogInCybLeuAspIleProAlaAspLeuProLeuCybHisThrValGly	67
Db	61	TCCAAGCCGCGCAGTCCCTTGGACATCCCTGCGGCACTGCCGCTTGTCCACACGGTGGC	120
OY	68	TyrlYsaIgmEArGleuProAsnLeuLeuGlnHisGluSerLeuAlaGluValLysGln	87
Db	121	TACAAAGGCATGGCGGCTGCCCAACTCTGTGAGACAGAGAGCCTGGCGGAATGAAGCAG	180
OY	88	GlnAlaSerSerTTPLeuProLeuLeuAlaLysArgCybHisSerAspThrGlnValPhe	107
Db	181	CAGCGAGCAGCTGGCTGGCCGCTGGCCAGCGCTGCCACTCGGATACGAGGCTTC	240
OY	108	LeuCybSerLeuPheAlaProValCybLeuAspArgProIleTyrProCybAspSerLeu	127
Db	241	CTGGTCTGCTCTTGTGGCGCGTGTGTGTGACCGGCGCACTTACCCGTCCGCTGCTG	300
OY	128	CysGluAlaValAlaArgAlaGlyCybAlaProLeuMetGluAlaTyrGlyPheProTyrPro	147
Db	301	TGGAGGCGCGTGGCGCGCGCTGGCGCGCTCATGAGAGGCTACAGGCTTCCCTGGC	360
OY	148	GluMetLeuHisCybHisLysPheProLeuAspAspLeuCybIleAlaValGlnPhe	167
Db	361	NN	420
OY	168	GlyHisLeuProAlaThrAlaProProValThrLysIleCybAlaGlnCybGluMetGlu	187
Db	421	NN	480
OY	188	HisSerAlaAspGlyLeuMetGluGlnMetCybSerSerAspPheValLysMetArg	207
Db	481	CACAGTCTGACGGCGCTCATGAGACAGATGTGCTCCAGTCACTTGTGGGTCAAAATGGCG	540
OY	208	IleLysGluIleLysIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLysLysLys	227
Db	541	ATCAAGAGATCAAGAATAGGAATGGGACCGGAAAGCTGATTGAGAGCCGAAAGAAAG	600
OY	228	LysLeuLeuLysPProGlyProLeuLysArgLysAspThrLysArgLeuValLeuHisMet	247
Db	601	AAGTGTCTCAAGCGGGCGCCCTCTGAAGCGCAAGACACCAAGGCGGTGGTGCACATG	660
OY	248	LysAsnGlyAlaGlyCybProCybProGlnLeuAspSerLeuAlaGlySerPheLeuVal	267
Db	661	AAGAAGCGCGCGGCTGCCCTCCCTGCCACAGCTGGACAGCTGGCGGGCAGCTTCCGTGCT	720
OY	268	MetGlyArgLysValAspGlyGlnLeuLeuMetAlaValTyrArgTyrAspLysLys	287
Db	721	ATGGGCGCGCAAGGTGATGAGACAGCTGCTCATGAGCCGTCTACCGCTGGGCAAGAAAG	780
OY	288	AsnLysGluMetLysPheAlaValLysPheMetPheSerTyrProCybSerLeuTyrTyr	307
Db	781	AATAAGAGATGAAGATTTCGCTCAATATCATATGTTCTTACCCCTGCTCTCTACTAC	840
OY	308	ProPhePheTyrGlyAlaAlaGluProHis	317
Db	841	CTTTTCTTCTTACGGGCGCGCAGAGCCCCAC	870
RESULT 5			
LOCUS	AY410885	799 bp DNA linear GSS 16-DEC-2003	
DEFINITION		Mus musculus SPBPS gene, VIRTUAL TRANSCRIPT, partial sequence,	
ACCESSION	AY410885		
VERSION	AY410885.1	GI:39766853	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 799)		

Pred. No.: 4,24e-125 Length: 819
 Score: 1335.00 Matches: 245
 Percent Similarity: 96.9% Conservative: 1
 Best Local Similarity: 96.5% Mismatches: 8
 Query Match: 77.2% Indels: 0
 DB: 7 Gaps: 0

US-10-768-566-1 (1-317) x CJ025307 (1-819)

QY 5 AAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuGluValAlaLeuHisTrp 24
 Db 58 GGGGGGGGAGGGGGGGGAGGGGGGGCTGGCTGGGGGGGGCTGGAGCGG 117
 QY 25 AlaProAlaArgCysGluGluValArgTrpGlyTrpGlnAlaGluProLeuHisGly 44
 Db 118 GCGCCGGGACACCGGCGAGGAGTACGACTACTAGCGGTGGAGACCGAGCGGTCGACAGG 177
 QY 45 ArgSerTrpSerLeuProProGlnCysLeuAspGlnProAlaAspLeuProLeuCysHis 64
 Db 178 CGCTGGTACTCCAAAGCGGCCCGGCTGAGATCCCGCGCACTGGCCACTCTGCAC 237
 QY 65 ThrValGlyTrpIlyAspArgLeuProAsnLeuGluGlnHisGluSerLeuAlaGlu 84
 Db 238 ACCGTGGGGTCAAAAGGCGATGGGGCTGCCCACTCTGGAGCAGAGAGCTGGCGAG 297
 QY 85 ValIlyGlnGlnAlaSerSerTrpLeuProLeuLeuAlaIlyAspCysHisSerAspThr 104
 Db 298 GTGAAACAGACAGCGGAGCGAGCTGGCTGCCCTGCGCAAGCGTGGCCACTCGACAG 357
 QY 105 GlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTrpCys 124
 Db 358 CAGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
 QY 125 ArgSerLeuCysGlnAlaValAlaArgAlaGlyCysAlaProLeuMetGlnAlaTrpGlyPhe 144
 Db 418 CGCTGCTTTCGAGAGGCGCGTGGCGCGCTGGCGCGCTGCTGAGAGCGTACGGCTTC 477
 QY 145 ProTrpProGluMetLeuHisCysHisIlyPhePheProLeuAspAsnAspLeuCysIleAla 164
 Db 478 CCTGGCCAGAGATGCTGCACTGCCCAAGTTCCCTCGAGACAAAGCTTCGATCGCT 537
 QY 165 ValGlnPheGlnHisIleuProAlaThrAlaProProValThrIlyIleCysAlaGlnCys 184
 Db 538 GTGCAATTTGGGAGCTGCGCCGCGCGCTCCAGTACCAAGATCTGGCGCCAGTAT 597
 QY 185 GluMetGlnHisSerAlaAspGlyLeuMetGlnGlnMetCysSerSerAspPheVal 204
 Db 598 GAGATGAGAGATGATGCCATGGCTCATGGAGCAATGTTTCCAGTACCTTCGATGTC 657
 QY 205 IlyMetArgIleIlyGlnIlyIleGlnAsnGlyAspArgIlyLeuIleGlyAlaGln 224
 Db 658 AAAATCGGCTCAAAAGATCAAGATAGAGATGGGAGACCGGAACTGATCGAGCCCA 717
 QY 225 Ily 244
 Db 718 AAAAAGAAAGAGTGTCTCAAGCGGGCGCCCTGAAACGCAAGGAGCAAGAGGCTGGTG 777
 QY 245 LeuHisMetLeuAsnGlyAlaGlyCysProCysProGlnLeu 258
 Db 778 CTGGCAATGAAGACGCTGCCGCTGCCCTGTGCCAGCTG 819

RESULT 7
 CK626659 635 bp mRNA linear EST 26-JAN-2004
 LOCUS m124f01.y1 Mouse RPE/choroid, unamplified: ml/mj Mus musculus cDNA
 DEFINITION
 ACCESSION CK626659.1 GI:41347545
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
 1 (bases 1 to 635)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Sclerognathi, Muroidea, Muridae, Murinae, Mus.
 Ida, H., Boylan, S., Weigel, A., Smit-McBride, Z., Chao, A., Gao, J.,
 Buchoff, P., Wistow, G., and Hjelmeand, L.
 Expressed sequence tag analysis of mouse RPE/choroid
 Unpublished (2004)
 CONTACT: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 24 row: F column: 01
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

1..635
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57Bl6J"
 /db_xref="taxon:10090"
 /clone_xref="m124f01"
 /sex="Male"
 /tissue_type="RPE/choroid"
 /dev_stage="Adult"
 /lab_host="EMD10B"
 /clone_lib="Mouse RPE/choroid, unamplified: ml/mj"
 /note="Organ: Eye; Vector: pSPoriT; 6ug total RNA was extracted from 200 adult male mouse RPE/choroid. A directionally cloned cDNA library in the pSPoriT vector(life technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTTCAGATCCGAGCGGCGCC(T)15-3'). cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:
 Pred. No.: 1.57e-101 Length: 635
 Score: 1102.00 Matches: 202
 Percent Similarity: 97.6% Conservative: 4
 Best Local Similarity: 95.7% Mismatches: 5
 Query Match: 63.7% Indels: 0
 DB: 7 Gaps: 0

US-10-768-566-1 (1-317) x CK626659 (1-635)

QY 84 GluValIlyGlnGlnAlaSerSerTrpLeuProLeuLeuAlaIlyAspCysHisSerAsp 103
 Db 2 GAGGTGAAGACAGGCAAGAGCTGCTGCCACTGCTGGGCCAAAGCTGCCACTCAAGAC 61
 QY 104 ThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTrpPro 123
 Db 62 ACCAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 QY 124 CysArgSerLeuCysGlnAlaValAlaArgAlaGlyCysValaProLeuMetGlnAlaTrpGly 143
 Db 122 TGGCGCTGCTGTGGAGCGGTGGCGCGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 QY 144 PheProTrpProGluMetLeuHisCysHisIlyPhePheProLeuAspAsnAspLeuCysIle 163
 Db 182 TTCCTTGGCCCGAATGCTGCACTGCGCAAGTTCCTCCCTGAGACAGACCTTGCATTC 241
 QY 164 AlaValGlnPheGlnHisIleuProAlaThrAlaProProValThrIlyIleCysAlaGln 183
 Db 242 GCGGTGCAATTTGGGCACTGCTGCCACCGCGCTCCAGTGAACCAAGATGTGTGCCAG 301
 QY 184 CysGluMetGlnHisSerAlaAspGlyLeuMetGlnGlnMetCysSerSerAspPheVal 203

Dn		302	TGTGAGATGGACACAGCGCTGATGCCCTCATGAAACAATGTGCTCCAGTGCATTTTTG	361
Oy		204	Vallysmetargilelyegluillelysalleguaengiyasparylisleullegiyla	223
Dd		362	GTCGAAGATGCCCATTAAGAAGATCAAGATVAGCAAACGGGGAACCGAAGATTGATTGAGACC	421
Oy		224	GlinysylsyblvlsleuleulyesProglyProleullyBaIglvsyaSpThrtilyaRlglen	243
Dd		422	CAGAGAAGAAAGAAACTCCTCAAGCACAGCCCCCTTTMAAGCGMACAGAACCAAMGAAGCTG	481
Oy		244	ValleunhsmetlcyasngilYalaglCySPProcypProginInteuspSerieleunlagly	263
Dd		482	GTCCTGCATAAGMAGNACGGGGCAAGCTGCCCTTCCCACATTAGACAACTTGACGGGC	541
Oy		264	SerphelenuvalMetGlYArglyVsAlaAgpyIglnLeuleuleumetalavalTyraRg	283
Dd		542	AGCTTCCTGGTCATGATGGCCGGAAAATGAGGGAGACGCTGCTGTCTCACGNGNSTCTAACCGC	601
Oy		284	TrpaaplyslvlsashnyeglUmetylpheala	294
Dd		602	TGGGCAAGAAAGAAATPAAGAGATGAAGTTTGCA	634
RESULT 8				
Locus BX715714				
DEFINITION	BX715714 XGC-tadpole Xenopus tropicalis cDNA clone TTPA040d06 5', mRNA sequence.	934 bp	mRNA linear	EST_18-NOV-2003
ACCESSION	BX715714			
VERSION	BX715714.1 GI:38388283			
KEYWORDS	Xenopus tropicalis (western clawed frog)			
SOURCE ORGANISM	Xenopus tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
REFERENCE AUTHORS	Xenopodinae; Xenopus; Silurana. 1 (bases 1 to 934) Croining,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,U. Sanger Xenopus tropicalis EST project 2001 (11_2003) Unpublished (2003) Contact: Croning MDR Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS SEQUENCE ID: TTPA040d06.plksp6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett. cDNA was oligo dt primed from sug of poly A+ RNA from tadpole embryos. EcoRI-NciI cut cDNA was then ligated into pcs107 with EcoRI at the 5' end and NciI at the 3' end. Vector: pcSI07, Site 1: EcoRI, Site 2: NotI Host: Escherichia coli DH10B. Location/Qualifiers 1..934 /organism=Xenopus tropicalis" /mol_type="mRNA" /db_xref=taxon:8364" /clone=TTPA040d06" /dev_stage=tadpole (stage 35-40)" /lab_host=E.coli DH10B" /clone.lib=XGC-tadpole" /note=vector: pcSI07, Site 1: EcoRI, Site 2: NotI; cDNA was oligo dt primed from sug of poly A+ RNA from tadpole embryos. EcoRI-NciI cut cDNA was then ligated into pcs107 with EcoRI at the 5' end and NotI at the 3' end"			
JOURNAL COMMENT				
FEATURES SOURCE				

Query Match:	Best Local Similarity:	72.9%	Mismatches:	31
DB:	US-10-768-566-1 (1-317) x BX715714 (1-934)	53.5%	Indels:	0
			Gaps:	0
QY	43	HiaglyAagserlyrserlyeProProglIncCyseAepilProAlaAspleuProheu	62	
Db	11	AACGACCGGTCTACTAACTAAATAGAGTCAGACAGACATCCCTCGGATCCATCTC	70	
QY	63	Cyshi8trVal1g1yTzlyArgMeCArgleuProAenLeuLeuGluhi8gluSerleu	82	
Db	71	TGCCATATATGTGGCTATATAAATAATGCAATGGCTATTTGTGTGACACAGAGCARTG	130	
QY	83	AlaGluVallygInGlnAlaSerSerTrpleuProLeuAlaAlayArGyshi8ser	102	
Db	131	CCTGAGGTGAAGCAGACAGCAGACAGCTGGGTGCTCTACTGCGCAACCGGTGCATCGA	190	
QY	103	AspPhrgInValPheLeuCyseSerleuPheAlaProValCyseleAspArgProIleTr	122	
Db	191	GATACTACGCTCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	250	
QY	123	ProCyAsrSerleuCyseGluAlaAlaValArgAlaGlyCyseAlaProLeuMetGluAlaTr	142	
Db	251	CCATGCGCGGTACTATAGAGAGTAGTGGGGACAGCTGTGCCCATCTATGAAATCCAT	310	
QY	143	GlyPheProTrProGluMetLeuHi8Cyshi8lyPhePheProLeuAspAsnAspleuCy	162	
Db	311	GGTTTCCCTTGGCCAGAGATGTTGAATGCAATTAATCCCTCTGATTAATGATCTGTGC	370	
QY	163	IleAlaValGlnPheGlyHi8leuProAlaThrAlaProProValThrly8IleCy8Ala	182	
Db	371	ATCACTGTCAGGTTTGGCAGCAAAACAGTCACTCAGCCACCAAGTACCAAGTTTGACT	430	
QY	183	GlnCy8GluMetGluHi8serAlaAspDlyLeuMetGluGlnMetCyseSerSerPhe	202	
Db	431	CAGGTGAAATAGAACACAGAGTCCGAAACATAGAGGGTGCACATTTTGGCAGTACATT	490	
QY	203	ValVallysmetCArgIlely8GluIlely8IleGluangIyAspArgly8leuIleGly	222	
Db	491	GTGCTACGAGATGCCGATTAAAGAAAGTTGAATGGAATGGAATGGAATGGAATGGAAT	550	
QY	223	AlaGlnly8ly8ly8ly8leuLeuLy8ProGlyProLeuLy8Argly8AspThrly8Arg	242	
Db	551	GCTCAGAAAGAAAGAAAGTCTCTCAAGACAGGAAAGCTMAAGAGAAAGAAATTCGCAAG	610	
QY	243	LeuValleuHi8Metly8AsnGlyAlaGlyCy8ProCy8ProGlnLeuAspSerleuAla	262	
Db	611	CTGGTCTCGATTAATTAAGAACCGCGCAAGTTGCCATATCTCTCAGCTGACCACTAAGT	670	
QY	263	GlySerPheLeuValMetGlyArgly8ValAspGlyInLeuLeuLeuMetAlaValTr	282	
Db	671	GGAAGCTTTCTTATCATGAGCGCCGTAAAGTGAACAATACTTTCTTACAGCCATCTAC	730	
QY	283	ArgTrpAspIly8ly8Asnly8GluMetly8PheAlaVally8PheMetPheSerTrPro	302	
Db	731	AAGTGGCAGCAAGAAAGCAAGATATAGACATGATGACGATTTCTATCTATCTATCA	790	
QY	303	CysSer 304		
Db	791	TGCTCT 796		
RESULT 9	BX719991	934 bp	mRNA	linear
LOCUS	BX719991			
DEFINITION	BX719991 XGC-tadpole Xenopus tropicalis cdna clone TTPA040d07 5',			
ACCESSION	BX719991			
VERSION	BX719991.1			
KEYWORDS	EST.			
SOURCE	Xenopus tropicalis (western clawed frog)			
ORGANISM	Xenopus tropicalis; Chordata; Craniata; Vertebrate; Euteleostomi;			

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 934)
AUTHORS
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE
Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL
Unpublished (2003)
COMMENT
Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPOCALIS SEQUENCE ID: TTPA040d07.plksp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NciI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NciI
Host: Escherichia coli DH10B.
Location/Qualifiers

FEATURES
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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TTPA040d07"
/dev_stage="tadpole (stage 35-40)"
/lab_host="E. coli DH10B"
/clone_lib="XGC-tadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NciI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NciI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:
Pred. No.: 1,14e-100 Length: 934
Score: 1096.00 Matches: 190
Percent Similarity: 88.2% Conservative: 41
Best Local Similarity: 72.5% Mismatches: 31
Query Match: 63.4% Indels: 0
DB: 5 Gaps: 0

US-10-768-566-1 (1-317) x BX719991 (1-934)

QY 43 HHSGLVATGSSerTyrSerIleProGlnGlyLeuAAspIleProAlaAspLeuProLeu 62
DB 11 AACGACCGCTTCTAATCAATAAGATCAATGATCAATGATCCCTTCGATCTCCATCTC 70
QY 63 CYSHisThrValGlyTyrIleValArgMetArgLeuProAsnLeuLeuGluHisGluSerLeu 82
DB 71 TGCCATATGTTGGCTATTAATAAATGCGATTGCTTAATTTGCTGACACAGACATG 130
QY 83 AAlaGluValLysGlnGlnAlaSerSerTyrLeuProLeuLeuAlaValArgCysHisSer 102
DB 131 CCTGAGGTGAACACCAAGCGACAGCTGGGCTCTACTGCGCAAGCGGTGCATCGA 190
QY 103 AAspThrGlnValPheLeuLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyr 122
DB 191 GATTACTCAAGCTCTTCTGCTCCCTTTTGTGCTCCATTGCTTGGAAAGACCCATTAT 250
QY 123 ProCysArgSerLeuLeuGlnAlaValArgAlaGlyCysAlaProLeuMetGlnAlaTyr 142
DB 251 CCATCCCGGTCACTATGCGAGGTAGTGGCGGACAGCTGCGCCAGTTATGGAATCCAT 310
QY 143 GlyPheProTyrProGlnLeuLeuHisCysHisValArgPheProLeuAspAsnAspLeuCys 162
DB 311 GGTTTCCCTTGGCCAGAGATGTTGAACCTGCATTAATTCCTTGTGATATGATCTGTGC 370
QY 163 IleAlaValGlnPheGlyHisIleuProAlaThrAlaProProValThrIleValIleCysAla 182
DB 371 ATCACTGTGCAGATTGGCAGCAACAGTCACTGACGCCACAGTGACCAAGATTGGACT 430

QY 183 GlnCysGlnMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPhe 202
DB 431 CAGTGTGAATTAAGACAGAACTCCGAACATGAGGGTGCACATTGTGCGAGTACTT 490
QY 203 ValValLysMetCysGlyIleValGluIleValIleGluHisGlnGlyAspArgLysLeuIleGly 222
DB 491 GTGCTACGATGCCCATTTAAAGAGTTAAGTTAAGATGAGATGAGATCGAAATCTATGCGCT 550
QY 223 AAlaGlnLysLysLysLysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArg 242
DB 551 GCTCAGAAAGAAAGAAAGAGTCTCCATAAGCAGGGAAGCTTAAAGAGAAAGAAATTCGCAAG 610
QY 243 LeuValLeuHisMetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAla 262
DB 611 CTGTTCTGTATTAATTAAGAACGCGCAAGTTGCCCATGCTCTCGATCGAACCTTAAGT 670
QY 263 GlySerPheLeuValMetGlyArgLysValAspGlyGlnLeuLeuLeuMetAlaValTyr 282
DB 671 GGAAGCTTTCTTATCATGCGCGCTAAGGTGACATTAATCTTCTTACAGCCATCTAC 730
QY 283 ArgTyrAspLysLysAsnLysGluMetLysPheAlaValLysPheMetPheSerTyrPro 302
DB 731 AAGTGGGACAAAGAAAGCAAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 790
QY 303 CysSer 304
DB 791 TGCTCT 796

RESULT 10

BO879095
LOCUS
DEFINITION
AGNCOURT_8124145 Lupsxl dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6178182 5', mRNA sequence.
BO879095
ACCESSION
BO879095.1 GI:22271103
VERSION
BO879095.1 GI:22271103
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 1026)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsrps-remail.nih.gov
Tissue Procurement: Dr. James R. Lupsxl
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM1357 row: F column: 07
High quality sequence start: 176
High quality sequence stop: 765.

FEATURES

source

1..1026
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6178182"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupsxl dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NciI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGGGTCCG-3' and
5'-GACTAGTTTATGATCGGAGCGGCCCTT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6,31e-99	Length:	1026
Score:	1079.50	Matches:	212
Percent Similarity:	88.7%	Conservative:	7
Best Local Similarity:	85.8%	Mismatches:	19
Query Match:	62.4%	Indels:	9
DB:	5	Gaps:	5

US-10-768-566-1 (1-317) x BQ879095 (1-1026)

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QY      1 MetATgAlaAlaAlaAlaAlaGlyValATgThAlAlaLeuAlaLeuLeuGly 20
DB      274 ATGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCGG 333
QY      21 AlaLeuHisThrAlaProAlaArgCysGluGluTyrAspTyrTyrGlyTrrGlnAlaGlu 40
DB      334 GCGCTGCACCTGGCGCGCGCGCGCTGCAGAGTACGACTACTATGCTGCAGCGCGCG 393
QY      41 ProLeuHisGlyArgSerTyrSerLysProProGlnCysLeuAspIleProAlaAspLeu 60
DB      394 CCGCTGCACGCGCGCGCTCTACTCCAGCGCGCGCGCGCGCGCTGCTGACATCCCTGCCACCTG 453
QY      61 ProLeuCysHisThrValGlyTyrTyrValArgMetArgLeuProAlaLeuLeuGlnHisGlu 80
DB      454 CCGCTGCACACACGCGTGGGCTTACAAGCGCATGCGCGCTGCCAACCTGTCGAGACGCGAG 513
QY      81 SerLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCys 100
DB      514 AACCTGCAGGAAGTGAAGACAGACGAGCAGCTGCTCCCTGCTGGCCAAAGCGCTGC 573
QY      101 HisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgPro 120
DB      574 CACTCGGATACGCAAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
QY      121 IleTyrProCysArgSerLeuCysGluAlaValArgAlaGlyCysAlaProLeuLeuGln 140
DB      634 ATCTACCGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
QY      141 AlaTyrGlyPheProTrpProGlnMetLeuHisCysHisLysPheProLeuAspAsnArg 160
DB      694 GCTACGCGCTTCCCTGCGCTGAGATGCTGCACTGCCACAAAGTTCCTCCCTGACAAACGAC 753
QY      161 LeuCysIleAlaValGlnPheGlyHisLeuProAlaThrAlaProProValThrLysIle 180
DB      754 CTCTGCATGCGCGCTGANTTCGGGACCTGCGCGCGCGCGCGCTGCTGATGACCAAGATC 813
QY      181 CysAlaGlnCysGluMetGlnHisSerAlaAspGlyLeuMetGlnGlnMetCysSerSer 200
DB      814 TCGCGCCAGTGGGAAGATGAGACAGCTGTAAGCGCTCATGGAACAAATGTCCTCCAG 873
QY      201 AspPheValValLysMetArgIleLysGlnLysIleGluAsnGlyAspA 218
DB      874 GACATTTTGGGCGCAAAATGCGGCATCCAGGAGATCCAGATAGAAAGATGGGGAGCC 933
QY      218 IglLysLeu---IleGlyAlaGlnLysLysLysLysLysLysLysLysLysLysLysLys 233
DB      934 GAAAGAGCTGGATTTGGAGCCCGCGCAAGAAAGAAAGAAAGAGAGCTGTGCTCCAGCCCGGCG 993
QY      234 --ProLeuLysArgLys 238
DB      994 GCCCCTGGAGAGCGC 1010
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RESULT 11

BP329572 593 bp mRNA linear EST 17-SBP-2004
LOCUS BP329572 Sugano cDNA library, rectum Homo sapiens cDNA clone
DEFINITION BP329572 Sugano cDNA library, rectum Homo sapiens cDNA clone

RC003796, mRNA sequence.
BP329572
VERSION BP329572.1 GI:52258756
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 593)
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES

source

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1..593
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RC03796"
/tissue_type="rectum"
/clone_id="Sugano cDNA library, rectum"
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ORIGIN

Alignment Scores:

Pred. No.:	9,26e-90	Length:	593
Score:	986.00	Matches:	181
Percent Similarity:	99.5%	Conservative:	1
Best Local Similarity:	98.9%	Mismatches:	1
Query Match:	57.0%	Indels:	0
DB:	3	Gaps:	0

US-10-768-566-1 (1-317) x BP329572 (1-593)

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QY      131 ValATgAlaGlyCysAlaProLeuMetGlnAlaTyrGlyPheProTrpProGlnMetLeu 150
DB      44 CTCCGCGCGCGCTGCGCGCGCGCTCATGAGGCTTACGCGCTTCCCTGCGCTGACATGCTG 103
QY      151 HisCysHisLysPheProLeuAspAsnArgCysIleAlaValGlnPheGlnHisLys 170
DB      104 CACTGCACCAAGTTCCTCCCTGACCAAGCCTTGCATGCGCGCTGCAATGGGCACTG 163
QY      171 ProAlaThrAlaProProValThrLysIleCysAlaGlnCysGluMetGlnHisSerAla 190
DB      164 CCGGCACCGCGCTTCCAGTACCAAGTCTGCGCGCGCGCTGATGAGACAGCACTGCT 223
QY      191 AspGlyLeuMetGlnGlnMetCysSerSerAspPheValValLysMetArgIleLysGlu 210
DB      224 GACGCGCTCATGAGACATGATGCTCCAGTACCTTGGTGCACAAATGCGCATCAAGAG 283
QY      211 IleLysIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLysLysLys 230
DB      284 ATCAAGATAGGAAGAGGAGACCGGAAGCTGTAGGCCCAAGAAAGAAAGAGCTGCTC 343
QY      231 LysPProGlyProLeuLysArgLysAspThrLysArgLeuValLysIleMetLysAsnGly 250
DB      344 AAGCGGGCGCGCTTGAACGCAAGACCAAGCGCGCTGCTGCTGCAATGAAATGGC 403
QY      251 AlaGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArg 270
DB      404 GCGGCGCTGCCCTGCGCAAGCTGGAAGCTGCGGAGGCACTTCTGTCATGAGGCGCG 463
QY      271 LysValaAspGlyGlnLeuLeuLeuMetAlaValTyrArgTrpAspLysLysLysLysLys 290
DB      464 AAGAGATGACAGACTGCTCTCATGCGCGCTTACCGCTGGAACAAAGAAATTAAGAG 523
```

QY 201 MetlyspheAlaVallyspheMetPheSerTyProCysSerLeuTyTyProPhephe 310
|||||
Db 524 ATGAAGTTTGACGATCAATTGATGTTCTCTCTACCCCTGCTCCCTCTACTACCCCTWTCCTC 583
QY 311 TTYTGTA1A 313
|||||
Db 584 TACGGGGCG 592

RESULT 12
CF982574 566 bp mRNA linear EST 18-DEC-2003
CF982574 maf55g06.y1 McCarrey Eddy 18 day preleptotene spermatocytes Mus
LOCUS mus55g06.y1 IMAGE:7030808 5' similar to TR:Q9W066 Q9W066
DEFINITION SECRETED FRIZZLED-RELATED PROTEIN 5. ; mRNA sequence.
ACCESSION CF982574
VERSION CF982574.1 GI:38515623
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurionathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 566)
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Page, D.,
Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagarishevili, R., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, J., Waterston, R. and Wilson, R.
NIHES Mouse
Unpublished (2002)
Contact: McCarrey/Eddy NIHES Mouse
NIHES Mouse
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: esewatson.wustl.edu
Library constructed and donated by J. McCarrey, Ph.D. (Southwest
Foundation for Biomedical Research, Dept. of Genetics) - excision
done by E. M. Eddy, Ph.D. (National Institutes of Health, National
Institute of Environmental Health Sciences).
Seq primer: Primer name ambiguous.
Location/Qualifiers
1. 566
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:7030808"
/sex="male"
/tissue_type="18-day preleptotene spermatocytes"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="McCarrey Eddy 18 day preleptotene
spermatocytes"
/note="Organ: testis; Vector: pBluescript SK-
(Stratagene); Site 1: XhoII; Site 2: EcoRI; CDNA oligo
dT-primed [5'-(GA)10-ACGATGCTCGAGTTTCTTTT-3'] and
directionally cloned using 5' linkers 5'-AATCGCACAG-3'
and 5'-CTCGGCGC-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XS) and resulting
single-stranded phagemids were prepiped and transformed into
DH10B. Library constructed and donated by J. McCarrey,
Ph.D. (Southwest Foundation for Biomedical Research, Dept.
of Genetics); excision done by E. M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences)."

ORIGIN
Alignment Scores:
Pred. No.: 4,866-87 Length: 566
Score: 959.00 Matches: 179
Percent Similarity: 96.8% Conservative: 4
Best Local Similarity: 94.7% Mismatches: 6
Query Match: 55.4% Indels: 1

DB: 7 Gaps: 0
US-10-768-566-1 (1-317) x CF982574 (1-566)

QY 104 ThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyPro 123
|||||
Db 1 ACCAGAGCTTCTCTGCTGCTGCTCTGCTCCGCTGCTGACCGACCACTATCACCCC 60
QY 124 CysArgSerLeuCysGluAlaValArgAlaGlyCysAlaProLeuMetGluAlaTyGly 143
|||||
Db 61 TGCGCGCTGCTGCTGGAAGCGGCTGCGCGCGGCTGCGCTGCTGATGAGGCGCTACGGT 120
QY 144 PheProTTPProGluMetLeuHisCysHisLeuPheProLeuAspAsnAspLeuCysIle 163
|||||
Db 121 TTCCTTGGCCCGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 164 AlaValGlnPheGlnHisLeuProAlaThrAlaProProValThrValIleCysAlaGln 183
|||||
Db 181 GCGGTGCACTTGGGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 184 CysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPheVal 203
|||||
Db 241 TGTGAGATGAGACACAGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 204 VallyMetArgIleLeuGluIleLeuGluLeuGluLeuGluLeuGluLeuGluLeu 223
|||||
Db 301 GTCAAGATGCCCATTAAGAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGAT 360
QY 224 GlnlySerlySlySlyLeuLeuLeuProGlyProLeuLySAspGlySAspThrLyArgLeu 243
|||||
Db 361 CAG 420
QY 244 ValLeuHisMetLySAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAlaGly 263
|||||
Db 421 GTCTCGATATGAG 480
QY 264 SerPheLeuValMetGlyArgLySAspGlyGlnLeuLeuLeuLeuLeuLeuLeuLeu 283
|||||
Db 481 AGCTTCCTGCTGATGAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 284 TTPAspLySAsnLySAsnLySAsnLySAsnLySAsnLySAsnLySAsnLySAsnLyS 292
|||||
Db 541 TGGAGCAGAGAA-ATTAAAGAGATGAAG 566

RESULT 13
CD673335 611 bp mRNA linear EST 24-JUN-2003
LOCUS fg23g02.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
DEFINITION fg23g02.y1, mRNA sequence.
ACCESSION CD673335
VERSION CD673335.1 GI:32175066
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 611)
Witow, G., Bernsteln, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
Mol. Vis. 8 (4), 185-195 (2002)
JOURNAL
PUBMED
12107412
Contact: Witow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 23 row: g column: 02

Seq primer: M13RP1 reverse primer (ABI).

Source

/mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="fg3902"
 /tissue_type="iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="human iris cDNA (Normalized): fg"
 /note="Organ: Eye; Vector: pcmspOR6; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded techniques in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-clones were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

1.1e-86	length:	611
956.00	Matches:	175
100.0%	Conservative:	0
100.0%	Mismatches:	0
55.3%	Indels:	0
6	Gaps:	0

US-10-768-566-1 (1-317) X CD673335 (1-611)

Qy	143	GlyPheProTrpProGluMetLeuHisCysHisIleValPheProLeuAspAsnArgLeuCys	162
Db	2	GGCTCCCTCCCTGAGATGGCTGACCTGCCCAAGATTCCTCCCTGGACACAGACTTGTGC	61
Qy	163	IleAlaValGlnPheGlyHisIleuProAlaThrAlaProProValThrLysIleCysAla	182
Db	62	ATGCGCGTGAGATTGGGGACCTGCGCCGACCGGCGCTTCAGTGAACCAAGATCTGGGCC	121
Qy	183	GlnCysGlnMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPhe	202
Db	122	CAGGTGAGATGGAGACACAGTGTGACGGCCCTCAAGAGACAGATGTGTCCAGAGACTTT	181
Qy	203	ValValIleMetArgIleIleuGluIleLysIleGluAsnGlyAspArgLysLeuIleGly	222
Db	182	GTGGTCAAATGGCGCATCAAGAGATCAAGATATAGAAATGGGGACCGGAAGCTGATTGGA	241
Qy	223	AlaGlnIleValLysLysLysLeuLeuLysProGlyProLeuLysValGlyValAspThrLysArg	242
Db	242	GCCACGAAAAAGAAAGAGCTGCTCAAGCCGGGCCCCCTGAAGCGCAGACCAACCAACGGG	301
Qy	243	LeuValLeuHisMetLysAsnGlyAlaGlyCysProCysProGlnIleLeuAspSerLeuAla	262
Db	302	CTGGTGTGTGACATGAAGAATGGCGGGAGTCCCTCCCTGCCACAGCTGGACAGCTGTGGC	361
Qy	263	GlySerPheLeuValMetGlyArgLysValIleAspGlyGlnLeuLeuLeuMetAlaValTyr	282
Db	362	GGCAGCTTCTTGATCATGGGCGGCAGAAAGTGAATGACACAGCTGTCTGTATATGGCCGTAC	421
Qy	283	ArgTrpAspLysLysAsnLysGluMetLysPheAlaValLysPheMetPheSerTyrPro	302
Db	422	CGCTGGGACAAAGAATAAGAGATGAAGTTTGACAGTCAATTCATGTCTCTCTACCCC	481
Qy	303	CysSerLeuTyrTyrProPhePheTyrGlyAlaAlaGluProHis	317
Db	482	TGCTCCCTCTACTACCTTTCTTCTTACGGGGGGGGCAGAGCCCCAC	526

RESULT 14

BP329610

LOCUS

DEFINITION

CONFIDENTIAL

ACCESSION

ACCESSION
NUMBER

VERSION

KEYWORDS

SOURCE

ORGANIS

3
4
5
6
7

DISCUSSION

REFERENCE

AUTHORS

TITLE

SECRET

ТОПНАТ

JOURNAL
DIRECTPUBMED
DOI:10.1002/ajb.10001

COMMENT

ЗАДАНИЕ

FEATURES

Source

ORIGIN

Alignment Scores:

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No.: 1.44e-85
: 945.00
nt Similarity: 96.3%
Local Similarity: 94.7%
Match: 54.6%
3
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US-10-768-566-1 (1-317) x BP329610 (1-606)

QY	131	ValArgAlaGlyCysAlaProIleuMetGluAlaTrgIysPheProTyrProGluMetLeu	150
Db	44	CTCCGGCGCGCGTCCGCGCGCTCATGGAGGCTTACGGCTTCCCTGGACTGAAATCTCG	103
QY	151	HisGlyHisIysPhePheProIleuAspAsnAspLeuCysIleAlaValAlaGlnPheGlyHisLeu	170
Db	104	CAGTGCACAAAGTTCCCTCTGGACAAACAGCTCTGACATGCCGCGTGCAGTTGGGCACTCG	163
QY	171	ProAlaThrAlaProProValThrIlysiIeCysAlaGlnCysGluMetGluHisSerAla	190
Db	164	CCGGCCACCGCGCGCTCCAGTGCACAAAGTTCGCGCCGATGTGAGATGAGACACAGTGCT	223
QY	191	AspGlyIleuMetGluGlnMetCysSerSerAspPheValValIlyIysMetAlaGlyIleIysGlu	210
Db	224	GACGGCGCTCATGGAGAGATGTGCTCCAGTGCATTGTGTGCACAAAGCCGATCAGAGAG	283
QY	211	IleIysIleGluIysnGlnIysAspArgIysLeuIleGlyAlaGlnIlyIysIysIysLeu	230
Db	284	ATCAAGATAGAAATGGAGACCGGAAAGCTGATTGAGCCCGAAGAAAAGAAAGACTCTCTC	343
QY	231	LysProGlyProLeuIlyAsnArgIysAspThrIlyAsnArgLeuValLeuHisIleMetIysAsnGly	250
Db	344	AAAGCCGGCGCCCTTGAAAGCGCAAGGACACAAAGCGGTGTGTGTGCACATGAAGAAATGCG	403
QY	251	AlaGlyCysPheProCysProGlnIleuAspSerLeuAlaGlySerPheLeuValMetGlyArg	270
Db	404	GCGGGCGTCCCGCCCAAGCTGCACAGCCTCGCGGGGCACTTCTGTGATATGGCCGC	463

Qy	271	LYSLVALAPGSLVGLNLEULEULEUWERLALVALTYRARGTTPAAPLYSLVSAASLLEGLU	290
Db	464	AAAGCGATGGACACACTCTCTCTCATGGCCGGCTACCCGCTCCGACAGAAAGATPAGAG	523
Qy	291	MELTYSPhEaLlAVALlYpPhMeLcPhESeRTYpProCYSeRLeUYTYr-PrOphE-PH	310
Db	524	ATGAAGCTTGAGTGCATTCATGTCTTCCTACCCCTGCTCTCCGTACTACCCCTTTCCTT	583
Qy	310	ETYrGLYAlA-AlAGLUDProHIS	317
Db	584	TACCGGGCGCGACAGCCCCAC	606
RESULT 15			
LOCUS	CD518814		
DEFINITION	AGENCOURT 14375702 NIH MGC 181 Homo sapiens cDNA clone	957 bp	mRNA linear EST 06-JUN-2003
ACCESSION	CD518814		
VERSION	CD518814.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 957)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Daniela S. Gerhard, Ph.D.		

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgcgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: NDAM492 row: 1 column: 03
High quality sequence stop: 488.

FEATURES	Location/Qualifiers
SOURCE	1. .957

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30408866"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/notes="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(deprecated); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

```

ORIGIN

Alignment Scores:

Pred. No.:	1.05e-81	Length:	957
Score:	910.00	Matches:	170
Percent Similarity:	89.6%	Conservative:	3
Best Local Similarity:	88.1%	Mismatches:	11
Query Match:	52.6%	Indels:	9
DB:	6	Gaps:	1

US-10-768-566-1 (1-317) X CD518814 (1-957)

```
QY      1 MetAArgAlaAlaAlaAlaAlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuLength 20
Db     100 ATGCGGGCGCGCGCGCGGGGGGGCGCGCGGACGGCCGCGCGCGCGCTGTCTGGGG 159
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QY	2	AlaLeuNI:ETPrAlaProAlaArgCysGlnGluTyrArgPyrTyrGlnYTTPGlnAlaGlu	40
Db	160	GCGCTGACATGGGCGCGCGCGCGCTGGCGAGAGATGACATCTATGGCTGGACGGCGAG	21.8
QY	41	ProLeuNI:SGLYAArgSerTyrSerIlysProProGlnCysIleuAaPrlleProAlaAaPrlleu	60
Db	220	CCGCTGACAGCGCGCTCTACTCCAAAGCGCGCGAGTGCCTTGAATCCCGCGCACTTG	27.9
QY	61	ProLeuCY:NI:ethrTAlaGlyTyrTyrAlaArgMetAlaGluProAlaIleuLeuGlnAlaGlu	80
Db	280	CCGCTCTGCCACCGGTGGGTACAAAGGACATGGCGCTGGCCAACTGGCTGGACACAG	33.9
QY	81	SerLeuAlaGlnValIysGlnGlnAlaSerSerTyrLeuProLeuLeuAlaIalysArgCys	100
Db	340	AGCCTGGCGGAAGTAGACAGACAGCGCGAGCTGGCTGGCGGCTGGCGCAACGCTGC	39.9
QY	101	HisSerAaPrlThrGlnValPheLeuCY:SerSerLeuPheAlaProValCY:IleuAaPrlArgPro	120
Db	400	CAGTGGAAATACGAGAGGCTTCTCTGGCTCGCTCTTTGGCGCGGCTGTCTGTACCGGGCC	45.9
QY	121	IleTyrProCY:ArgSerSerLeuCY:SGlnAlaValAlaAlaGlyCY:ValAProLeuMetGln	140
Db	460	ATTAACCCGCGCGCGCTCGCTGGCGAGGCGCGGCGCGCGCTGGCGGCGCTGATGAG	51.9
QY	141	AlaTyrGlyPheProTyrProGlnMetLeuNI:ScyShiIlys-PheProLeuAaPrlaAs	160
Db	520	GCTTACCGCTCCCCCTGGCTGAGATGCGGACATGCCACAAAGTTTCCCCCTGGCAACGA	57.9
QY	160	PleuCY:IIeAlaValAlaGlnPheGly-----HisLeuProAl	172
Db	580	CCCTGGATGCGCGTGCAGATTGCGGGAGACTGACCGCGTACCGCGGCGCGAGTTGACCA	63.9
QY	172	ethrAlaProProValThrIlysIleCY:AlaGlnCys	184
Db	640	GATTTGGCCCCAGGTGTGAGTGAAGACACCTTTGC	676

Search completed: March 23, 2006, 08:19:42
Job time : 4515 Secs

Job time : 4515 sec

GenCore version 5.1.7
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OW protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 07:05:30 ; Search time 904 Seconds
(without alignments)
2899.771 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGVYRTAALALILG.....MFSYPCSLYPPFYGAAPH 317

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODL=frame+ p2n.model -DEV=xlh
-Q=/abse/ABSSWB_Spool/US10768566/runat_22032006_155813_25385/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1
-MATRIX=bloum62 -TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEASize=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abse02h
-USER=US10768566@cgn1_1_1026 @runat_22032006_155813_25385 -NCPUs=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main:*

No.	Score	Query Match	Length	ID	Description
1	1730	100.0	954	US-10-338-604-3	Sequence 3, Appli
2	1730	100.0	1905	US-10-338-604-1	Sequence 1, Appli
3	1730	100.0	1905	US-10-768-566-2	Sequence 2, Appli
4	1730	100.0	1984	US-10-146-474-5	Sequence 5, Appli
5	1730	100.0	1984	US-10-301-764-5	Sequence 4, Appli
6	1613	93.2	945	US-10-338-604-6	Sequence 6, Appli
7	1613	93.2	1186	US-10-338-604-4	Sequence 4, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	ID	Description
8	924.5	53.4	1308	US-10-146-474-18	Sequence 18, Appli
9	924.5	53.4	1308	US-10-301-764-18	Sequence 18, Appli
10	924.5	53.4	2078	US-10-138-434A-1	Sequence 1, Appli
11	924.5	53.4	2094	US-10-756-149-3306	Sequence 3306, Ap
12	924.5	53.4	2602	US-10-666-851-1	Sequence 1, Appli
13	924.5	53.4	4500	US-10-138-434A-27	Sequence 27, Appli
14	917	53.0	942	US-10-425-586-2	Sequence 2, Appli
15	917	53.0	942	US-10-466-136-2	Sequence 2, Appli
16	917	53.0	1017	US-10-425-586-9	Sequence 9, Appli
17	916	52.9	2075	US-10-138-434A-2	Sequence 2, Appli
18	916	52.9	2075	US-10-425-586-1	Sequence 1, Appli
19	916	52.9	2075	US-10-466-136-1	Sequence 1, Appli
20	916	52.9	4462	US-09-974-298-28	Sequence 28, Appli
21	916	52.9	4469	US-09-796-008-1	Sequence 1, Appli
22	916	52.9	4469	US-10-133-937-42	Sequence 42, Appli
23	916	52.9	4469	US-10-132-118-857	Sequence 857, App
24	916	52.9	4469	US-10-159-563-82	Sequence 42, Appli
25	916	52.9	4469	US-10-342-887-857	Sequence 857, App
26	916	52.9	4469	US-10-786-720-15	Sequence 15, Appli
27	916	52.9	4469	US-10-788-792-21	Sequence 21, Appli
28	916	52.9	4469	US-10-473-974-203	Sequence 203, App
29	916	52.9	4469	US-10-817-525-1	Sequence 1, Appli
30	714	41.3	804	US-10-425-586-12	Sequence 12, Appli
31	659	38.1	741	US-10-425-586-11	Sequence 11, Appli
32	625	36.1	885	US-09-934-483A-2	Sequence 2, Appli
33	625	36.1	1799	US-09-934-483A-3	Sequence 3, Appli
34	625	36.1	1859	US-09-934-483A-4	Sequence 4, Appli
35	625	36.1	2030	US-10-146-474-1	Sequence 1, Appli
36	625	36.1	2030	US-10-301-764-1	Sequence 1, Appli
37	624	36.1	1380	US-10-783-528-49	Sequence 49, Appli
38	624	36.1	1382	US-10-295-027-1128	Sequence 1128, Ap
39	624	36.1	1382	US-10-473-974-197	Sequence 197, App
40	624	36.1	1988	US-10-177-293-141	Sequence 141, App
41	624	36.1	2027	US-08-949-904-1	Sequence 1, Appli
42	621.5	35.9	2379	US-09-925-065A-678403	Sequence 678403,
43	620	35.8	2085	US-10-106-698-2105	Sequence 2105, Ap
44	616	35.6	1869	US-09-981-876-56	Sequence 56, Appli
45	616	35.6	1869	US-09-148-545-56	Sequence 56, Appli

ALIGNMENTS

RESULT 1
US-10-338-604-3
; Sequence 3, Application US/10338604
; Publication NO. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE REFERENCE: MPT01-250PIRM
; CURRENT APPLICATION NUMBER: US/10/338, 604
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-338-604-3

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
2.04e-205	1730.00	317	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0

US-10-768-566-1 (1-317) x US-10-338-604-3 (1-954)

QY 247 MetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeu 266
DB 730 ATGAAGAAAGGGGCAAGCTGCGCTTCCACATTGACCACTGACGGGAGCTTCTCG 789
QY 267 ValMetGlyArgLysValAspGlyGlnLeuLeuMetAlaValTyrTrpGlyPheLys 286
DB 790 GTCATGGGGCGGCAAGTGAAGGACAGCTGCTGACCGCGCTTACCGCTGGAGCAAG 849
QY 287 LysAsnLysGluMetLysPheAlaValLysPheMetPheSerTyrProCysSerLeuTyr 306
DB 850 AAGATTAAAGAGATGAAGTTTGGGTCAATTCTTCTCTATCCCTGTTCCCTTAC 909
QY 307 TyrProPhePheTyrGlyAlaAlaGluProHis 317
DB 910 TACCTTTTCTATGGGCGAGCTGAACCCAC 942
RESULT 7
US-10-338-604-4
; Sequence 4, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; TITLE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (242) ... (1186)
US-10-338-604-4
Alignment Scores:
Pred. No.: 1,166-190 Length: 1186
Score: 1613.00 Matches: 295
Percent Similarity: 96.5% Conservative: 5
Best Local Similarity: 94.9% Mismatches: 11
Query Match: 93.2% Indels: 0
Gaps: 0
DB: 6
US-10-768-566-1 (1-317) x US-10-338-604-4 (1-1186)
QY 7 AlaGlyGlyValArgThrAlaAlaLeuAlaLeuLeuGlyAlaLeuHisTrpAlaPro 26
DB 251 GCTTGAGGCGCACGAGCGGCGGACTGCGGTGCTGCTCGGGCGCTGATGGGCGCA 310
QY 27 AlaArgCysGluGluTyrAspTyrTyrGlyTyrGlnAlaGluProLeuHisGlyArgSer 46
DB 311 ACAACGGCGCCAGAGTACGACTACGCTTGGCAGCGGACCGCTGACCGCGCTCC 370
QY 47 TyrSerLysProProGlnCysLeuAspLleProAlaAspLeuProLeuCysHisThrVal 66
DB 371 TACTCCAAAGCCACCGGAGTGCCTCGACATCCCGCGGATCTGCTGTGACACGCTG 430
QY 67 GlyTyrLysArgMetArgLeuProAlaLeuGluHisGluSerLeuAlaGluValLys 86
DB 431 GGTCTCAAGCGCATGGGCTGCCCACTGCTGAGACAGAGGCTGGCCGAGGTGAAG 490
QY 87 GlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCysHisSerAspThrGlnVal 106
DB 491 CAGCAGGCGCAGCAGCTGCTGCACCTGCTGGCAGCGCTGCCACCTCAGACCCAGGTC 550
QY 107 PheLeuCysSerLeuPheAlaProValCysLeuAspArgProLleTyrProCysArgSer 126

DB 551 TTCCTGCTGCTCTTCTGCTCCCTGCTGCTGACGACCCATTTACCCCTGCGCTCG 610
QY 127 LeuCysGluAlaValArgAlaGlyCysAlaProLeuMetGluAlaTyrGlyPheProTrp 146
DB 611 CTGTGCGAAGCTGGCGCGCGGCTGCGCTCGGCTCATGAGGCGCTTACGGTTCTCCCTGG 670
QY 147 ProGluMetLeuHisCysHisLysPheProLeuAspAsnAspLeuCysIleAlaValGln 166
DB 671 CCGGAGATGCTGCATCGCACAAAGTTCCCTGACCAAGACCTCTGATGCGGTGAG 730
QY 167 PheGlyHisLeuProAlaThrAlaProProValThrLysIleCysAlaGlnCysGluMet 186
DB 731 TTGGGGACCTGCTCGCCACCGCGCTCATGACCAAGATCTGTGCCAGTGTAGATG 790
QY 187 GluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAspPheValValLysMet 206
DB 791 GAGCAGACGGCTGACGGCTCATGAGACAGATGCTCATGATCTTGTGGTCAAGATG 850
QY 207 ArgIleLysGluIleLysIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLysLys 226
DB 851 CGCATTTAAGAGATCAAGATAGACAAACGGGACCGAAAGTTGATTGAGAGCCAGAAAG 910
QY 227 LysLysLeuLeuLysProGlyProLeuLysArgLysAspThrLysArgLeuValLeuHis 246
DB 911 AAGAACTGCTCAAGCGAGCGCCCTTAAAGCGCAAGACCAAGAACTGTCTGCAAT 970
QY 247 MetLysAsnGlyAlaGlyCysProCysAspProGlnLeuAspSerLeuAlaGlySerPheLeu 266
DB 971 ATGAAGAAAGGGGCAAGCTGCGCTTCCACATTTAGCAACCTGACGGGAGCTTCTCG 1030
QY 267 ValMetGlyArgLysValAspGlyGlnLeuLeuMetAlaValTyrArgTrpAspLys 286
DB 1031 GTCATGGGCGGCAAGTGAAGGAGGACAGCTGCTGACGCGCTTACCGCTGGAGCAAG 1090
QY 287 LysAsnLysGluMetLysPheAlaValLysPheMetPheSerTyrProCysSerLeuTyr 306
DB 1091 AAGAAATTAAGAGATGAAGTTGGGTCAAAATTCATGTTCTCTATCCCTGTTCCCTTAC 1150
QY 307 TyrProPhePheTyrGlyAlaAlaGluProHis 317
DB 1151 TACCTTTTCTATGGGCGAGCTGAACCCAC 1183
RESULT 8
US-10-146-474-18
; Sequence 18, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umaneky, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,474
; FILING DATE: 14-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:


```

Qy      235  LeuLysArgbysaphrlyrbsArgLeuValIleuHleMetIysAsnDyIaIagIyCysPro 254
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1013 ATCAAGAGAGAGACCTCGAAGAGCTTGTCTCTACTGAGAGATGGGCTACTGTCCC 1072
Qy      255  CysProGlnLeuAspSerIleuAlaGlySerPheLeuValMetGlyArgIysValAspGly 274
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1073 TGCACACAGCTGGACAACCTCAGCCACCACTTCTCATCATCATGAGCGCGAAGGAGAC 1132
Qy      275  GlnLeuLeuMetAlaValTyrArgTTPAspIlyIysAsnIysAsnIleuMetIysPheAla 294
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1133 CAGTACTTGTGTGACGGCCATCCCAAGTGGAGCAAGAAAAACAAGAGATTCAAAAACTTC 1192
Qy      295  ValIysPheMetPheSerTyrProCysSerLeuTyrTyrProPhePhe 310
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1193 ATGAGAAAAATGAAAAACCATGAGTCCCACTTTCAGTCCGTGTTT 1240

RESULT 9
US-10-301-764-18
Sequence 18, Application US/10301764
Publication No. US20040039184A1
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,764
FILING DATE: 20-No. US20040039184A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-301-764-18

Alignment Scores:
Pred. NO.: 1.44e-104 Length: 1308
Score: 924.50 Matches: 179
Percent Similarity: 72.8% Conservative: 51
Best Local Similarity: 56.6% Mismatches: 77
Query Match: 53.4% Indels: 9
DB: 7 Gaps: 6
US-10-768-566-1 (1-317) x US-10-301-764-18 (1-1308)

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US-10-768-566-1 (1-317) x US-10-666-851-1 (1-2602)

QY 1 MetArgAlaAlaAlaAlaGlyValArgThrAlaAlaLeuLeu----- 18
Db 119 ATGGGCGATCGGCGCGAGGAGGAGGCGCGCGCGGAGGCCCTGGGCGCTGCGGCG 178
QY 19 LeuGlyAlaLeuHisThrAlaProAlaArgCysGluGluTyrArgTyrTyrGlyTyrGln 38
Db 179 CTGGGCGCGGCGCTTGGCGGCTGGGCGCTGGCGCGAGTACGACTACGTGACCTTCCAG 238
QY 39 AlaGlu-----ProLeuHis--GlyArgSerTyrSerTyrProProGlnCysLeuAsp 55
Db 239 TCGGACATCGGCGCGTACAGAGCGGCGGCTTCTTACACCAAGCCACTCAGTGGTGGAC 298
QY 56 IleProAlaAspLeuProLeuCysHisThrValGlyTyrValAspMetArgLeuProAsn 75
Db 299 ATCCCGCGGAGCTGGCGGCTGGCCACAACTGGAGCTTACAAAGAAATGCTGGCCCAAC 358
QY 76 LeuLeuGluHisGluSerLeuAlaGluValLysGlnGlnAlaSerSerTyrLeuProLeu 95
Db 359 CTGCTGGAGCAGAGACCATGCGGAGGTGAAGCAGACGAGCCAGACTGGGTGCTCCCTG 418
QY 96 LeuAlaLysArgCysHisSerAspThrGlnValPheLeuCysSerLeuPheAlaProVal 115
Db 419 CTCAACAAGAACTGGCAGCGCGAGCCAGAGTCTTCTGCTGCTGCTTGGCGCCGCTG 478
QY 116 CysLeuAspArgProIleTyrProCysArgSerLeuCysGluAlaValArgAlaGlyCys 135
Db 479 TGCCTGGACCGGCGCATCTACCCGTCGCTGGCTGGCGAGGCGCTGGCGAGCTCGTG 538
QY 136 AlaProLeuMetGluAlaTyrGlyPheProTyrProGluMetLeuHisCysHisLeuPhe 155
Db 539 GAGCGCGGTCACTGCACTTCTGGCGCTTCACTGCGCCAGAGAGCTTAAGTGCACAACTTC 598
QY 156 ProLeuAspAsnAspLeuCysIleAlaValGlnPheGlyHis--LeuProAlaThrAla 174
Db 599 CCC---GAGGGGAGCTGTGCATCGCCATGACGCGCCCAATGGCACCGAAGCCTCCAG 655
QY 175 ProProValThrIlyIleCysAlaGlnGlyMetGluHisSerAlaAspGlyLeuMet 194
Db 656 CCCAAGGACAAACGCTGTGCTCCCTCTGTGACAAACGATGTAATCTGAGGCCATCATTT 715
QY 195 GluGlnMetCysSerSerAspPheValLysMetArgIleLysGluIleLysIleGlu 214
Db 716 GAACATCTCTGTGCCAGGAGTTTGCATGTAGAGTAATAATTAAGAAGTGAATAAAGAA 775
QY 215 AsnGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLysLeuLeuLysPyrGlyPro 234
Db 776 AATGCGCAGAAAGATTGTC-----CCCAAGAAAGAAAGCCCTGAAATTTGGGGGCC 829
QY 235 LeuLysAspArgLysAspThrLysArgLeuValLeuHisMetLysAsnGlyAlaGlyCysPro 254
Db 830 ATCAAGAAGAAAGACCTGAAGAGCTTGTGCTGTAACCTGAAGAAATGGGGCGTACCTCC 889
QY 255 CysProGlnLeuAspSerSerLeuAlaGlySerPheLeuValMetGlyArgLysValAspGly 274
Db 890 TGGCACCAAGCTGGACAACTCAGCCACCACTTCCATCAATGAGGCGGCAAGCTGAAGGC 949
QY 275 GlnLeuLeuLeuMetAlaValTyrArgTyrAspLysLysLysLysLysLysLysPheAla 294
Db 950 CAGTACTTGTGACCGCGCATCCACAAAGTGGGACAAAGAAACAAAGAGTTCATAAAATTC 1009
QY 295 ValLysPheMetPheSerTyrProCysSerLeuTyrTyrProPhePhe 310
Db 1010 ATGAAGAAATGAATAAACCATGAGTGCACCTTCACTCCGCTTT 1057

RESULT 13
US-10-138-434A-27
; Sequence 27, Application US/10138434A
; Publication No. US20030175864A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE

APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
 APPLICANT: Rubin, Jeffrey S.
 APPLICANT: Finch, Paul
 APPLICANT: Aaronson, Stuart
 APPLICANT: He, Xi
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF
 FILE REFERENCE: 4239-62570
 CURRENT APPLICATION NUMBER: US/10/138,434A
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US 09/087,031
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: US 60/050,495
 PRIOR FILING DATE: 1997-06-23
 PRIOR APPLICATION NUMBER: US 60/050,417
 PRIOR FILING DATE: 1997-05-29
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 27
 LENGTH: 4500
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-138-434A-27

Alignment Scores:
 Pred. No.: 8,43e-104 Length: 4500
 Score: 924.50 Matches: 179
 Percent Similarity: 72.8% Conservative: 51
 Best Local Similarity: 56.6% Mismatches: 77
 Query Match: 53.4% Indels: 9
 Gaps: 6

US-10-768-566-1 (1-317) X US-10-138-434A-27 (1-4500)

[illegible]

Job time : 915 secs

Percent Similarity: 74.1%
Best Local Similarity: 57.9%
Query Match: 53.0%

Conservative: 50
Mismatches: 70
Indels: 10
Gaps: 7

US-10-768-566-1 (1-317) x US-10-466-136-2 (1-942)

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QY      8 GlyGlyValArgThrAlaLeuAlaLeuLeuGlyAlaLeuHisTrpAlaProLa 27
DB      22 GGGGGCGCGCGCGGCGAGCCCTGGGCGTGTCTG--GCCTGGGCGCGCTTCTGGC 78
QY      28 Arg-----CysGluGluTrpAspTyrTyrGlyTrpGlnAlaGlu-----ProLeuHis 43
DB      79 CGTGGGCTGGCAGCAGATACGACTGAGAGCTTCAGTCCAGTCCGAGATCGGCCGTACAG 138
QY      44 ---GlyArgSerTyrSerIleProGlnCysLeuAspIleProAlaAspLeuProLeu 62
DB      139 AGCGGGCGCTTCTTACACCAAGCCACTTCAGTGGTGAACATCCCCGAGACTCGGGCTG 198
QY      63 CysHisThrValGlyTyrLysArgMetArgLeuProAsnLeuGluHisGluSerLeu 82
DB      199 TGCACAACAGTGGGCTACCAAGAAGATGTGTGCTGCCAAGCTGTGAGCAGACCATG 258
QY      83 AlaGluValIleGlnAlaSerSerTrpLeuProLeuAlaLysArgCysHisSer 102
DB      259 GCGAGGTGAGAGCAGCAGCAGCAGCTGCTGCTCTCAACAAAGAACTGCCAGGCC 318
QY      103 AspThrGlnValPheLeuCysSerLeuPheAlaProValCysLeuAspArgProIleTyr 122
DB      319 GGGACCCAGTCTTCTCTGCTGCTCTGCTCTGCGCCCTGCTGCTGAGACCGGCCATCTAC 378
QY      123 ProCysArgSerLeuCysGluAlaValArgAlaGlyCysAlaProLeuMetGluAlaTyr 142
DB      379 CCGTGTGCTGGTGTGCGAGCGCGTGGCGAGCTCGTGGAGCGCGTCAATGCACTTCTC 438
QY      143 GlyPheProTrpProGluMetLeuHisCysHisLysPhePheProLeuAspAsnAspLeuCys 162
DB      439 GGCCTTCTACTGGCCCGAGATGCTTAAGTGTGACAACTCCCG--GAGGGGGAGCTGTGC 495
QY      163 IleAlaValAlaGlnPheGlyHis---LeuProAlaThrAlaProProValThrLysIleCys 181
DB      496 ATGCGCATAGCGCGCCCAATGCGCCAGCCAGGCTCCAGGCCCAAGGCAACAGCGTGTG 555
QY      182 AlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSerAsp 201
DB      556 CTTCCCTGTGACACAGATGTAATGAGGCCCATTTGAACATCTGTGTGCCAGCAG 615
QY      202 PheValValIleMetArgIleLysGluIleLysIleGluAsnGlyAspArgLysLeuIle 221
DB      616 TTTCACACTGAGATGAATAAATAAAGAAATGAAAAAATGCGACAAAGAAATTTGTC 675
QY      222 GlyAlaGlnLysLysLysLysLeuLysPheGlyProLeuLysArgLysAspThrLys 241
DB      676 -----CCCAAGAAAGAAAGCCCTGAGAGTTGGGGCCCATCAAGAAAGAGACTGAG 729
QY      242 ArgLeuValLeuHisMetLysAsnGlyAlaGlyCysProCysProGlnLeuAspSerLeu 261
DB      730 AAGCTTGTGTGTAAGTGAAGATGGGGCTGACTGTCTCCGCAACGAGCTGGACAACCTC 789
QY      262 AlaGlySerPheLeuValMetGlyArgLysValAspGlyGlnLeuLeuMetAlaVal 281
DB      790 AGCCACCACTTCTCTCATCTGAGCGCCCAAGGTGAAGAGCCAGTACTTGTGACGGCCATC 849
QY      282 TyrArgTrpAspLysLysLysLysGluMetLysPheAlaValLysPheMetPheSerTyr 301
DB      850 CACAAGTGGACAAAGAAACAAAGAGTTCAAAAACTTCATGAAGAAATGAAAAACAT 909
QY      302 ProCysSerLeuTyrTyrProPhePhe 310
DB      910 GAGTGCCCACTTTCAGTCCGTGTTT 936
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Search completed: March 23, 2006, 07:20:54

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus.p2n model

Run on: March 23, 2006, 07:05:10 ; Search time 390 Seconds
(without alignments)
1895.258 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730
Sequence: 1 MRNAAAAGVRRPALALLG.....MFSYPCSDYPPFYGAEPH 317

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=200000000 -HOST=abs04
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-NO_WAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_NA_New.*

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6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	52.9	4469	9	US-11-245-147-203
2	916	52.9	4608	8	US-10-821-234-137
3	624	36.1	1382	9	US-11-245-147-197
4	621.5	35.9	2379	6	US-09-925-065A-678403

5	615.5	35.6	926	9	US-11-245-147-5	Sequence 5, Appli
6	457	26.4	872	9	US-11-245-147-80	Sequence 80, Appl
7	453	26.2	495	12	US-11-004-762-19	Sequence 19, Appl
8	434	25.1	631	6	US-09-925-065A-68204	Sequence 68204, A
9	420.5	24.3	1745	9	US-11-051-720-28	Sequence 28, Appl
10	285	16.5	1291	12	US-11-184-005-23	Sequence 23, Appl
11	283.5	16.4	2374	12	US-11-184-005-1	Sequence 1, Appl
12	280	16.2	2184	12	US-11-054-281-35	Sequence 35, Appl
13	279.5	16.2	1484	12	US-11-184-005-3	Sequence 3, Appl
14	276	16.0	2561	12	US-11-127-877-26	Sequence 26, Appl
15	269	15.5	2811	12	US-11-067-531-154	Sequence 154, Appl
16	269	15.5	2814	12	US-11-054-281-21	Sequence 21, Appl
17	268.5	15.5	1935	12	US-11-136-527-186	Sequence 186, Appl
18	267	15.4	1983	9	US-11-245-147-206	Sequence 206, Appl
19	263.5	15.2	1944	9	US-11-245-147-49	Sequence 49, Appl
20	263	15.2	4350	9	US-11-245-147-124	Sequence 124, Appl
21	263	15.2	4350	9	US-11-245-147-125	Sequence 125, Appl
22	263	15.2	4350	9	US-11-245-147-205	Sequence 205, Appl
23	253.5	14.7	7391	12	US-11-152-366-17	Sequence 17, Appl
24	253.5	14.7	7391	12	US-11-169-041-5	Sequence 5, Appl
25	253.5	14.7	7392	9	US-11-245-147-177	Sequence 177, Appl
26	253.5	14.7	7392	9	US-11-245-147-208	Sequence 208, Appl
27	250	14.5	4770	12	US-11-136-527-299	Sequence 299, Appl
28	247	14.3	1898	12	US-11-136-527-2690	Sequence 2690, Ap
29	226.5	13.1	1076	12	US-11-128-061-1138	Sequence 1138, Ap
30	226.5	13.1	1076	12	US-11-128-049-1138	Sequence 1138, Ap
31	210.5	12.2	2607	12	US-11-136-527-630	Sequence 630, Appl
32	207	12.0	2820	9	US-11-245-147-204	Sequence 204, Appl
33	207	12.0	2820	12	US-11-186-284-188	Sequence 188, Appl
34	207	12.0	2840	12	US-11-054-281-23	Sequence 23, Appl
35	206	11.9	3375	9	US-11-245-147-178	Sequence 178, Appl
36	206	11.9	3375	9	US-11-245-147-207	Sequence 207, Appl
37	161	9.3	4804	12	US-11-067-811-3	Sequence 3, Appl
38	156	9.0	6004	12	US-11-136-527-5450	Sequence 5450, Ap
39	156	9.0	604	12	US-11-136-527-1354	Sequence 1354, Ap
40	150	8.7	1166	8	US-10-750-185-38928	Sequence 38928, A
41	150	8.7	1166	8	US-10-750-623-38928	Sequence 38928, A
42	149.5	8.6	1853	8	US-10-750-185-51334	Sequence 51334, A
43	149.5	8.6	1853	8	US-10-750-623-51334	Sequence 51334, A
44	130	7.5	1302	12	US-11-152-366-18	Sequence 18, Appl
45	119.5	6.9	1815	8	US-10-750-185-48508	Sequence 48508, A

ALIGNMENTS

RESULT 1
US-11-245-147-203
; Sequence 203, Application US/11245147
; Publication No. US20060030541A1
GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALI, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAMADI, GEORGES
TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
FILE REFERENCE: 37991-0023
CURRENT APPLICATION NUMBER: US/11/245,147
CURRENT FILING DATE: 2005-10-07
PRIOR APPLICATION NUMBER: PCT/IB02/02211
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/281,400
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 203
LENGTH: 4469
TYPE: DNA
ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: Homo sapiens secreted frizzled-related protein 1
; OTHER INFORMATION: (SPRP1), mRNA.
US-11-245-147-203

Alignment Scores:
Pred. No.: 8,37e-75 Length: 4469
Score: 916.00 Matches: 179
Percent Similarity: 72.0% Conservative: 50
Best Local Similarity: 56.3% Mismatches: 77
Query Match: 52.9% Indels: 12
DB: 9 Gaps: 7

US-10-768-566-1 (1-317) x US-11-245-147-203 (1-4469)
QY 2 ArgAlaAlaAlaAlaAlaGly-----GlyValArgThrAlaAlaLeuAlaLeu 18
DB 24 AGAGCCGGCATGGGCGATCGGGCGCAGCGAGGGGGCGCGGGGGCGCTGGGGCTGCTG 353
QY 19 -----LeuGlyAlaLeuH1eTPrAlaProAlaArgCyGluGluLysAspTYTYrgly 36
DB 354 CTGGGCGTGGGGCGGGCGCTTCTGGCCGTGGGCTGGCCAGGAGTACGACTACGTGAGC 413
QY 37 TrgAlaAlaGlu-----ProLeuH1s---GlyArgSerTYrSerLysProProGlnCy 53
DB 414 TTCAGTGGACATGGCGCCCGTACAGAGCGGGCGCTTCTACAGCAGCCAGCTCAGTGC 473
QY 54 LeuAspIleProAlaAspLeuProLeuCyGlnH1eTPrValGlyTYrLysArgMetArgLeu 73
DB 474 GTGGACATCCCGCGGACCTGGGGCTGTGCCAGACGTGGGGCTTCAAGAAATGTGCTG 533
QY 74 ProAsnLeuLeuGluH1eGluSerLeuAlaGluValLysGlnGlnAlaSerSerTPrLeu 93
DB 534 CCCAAGCTGTGTGAGCAGACAGACCATGTGGGAGGTGAAGCAGACAGCGCGTGGGTG 593
QY 94 ProLeuLeuAlaLysArgCyGlnH1eSerAspThrGlnValPheLeuCySerLeuPheAla 113
DB 594 CCCGCTCTCAAGAAACTGCGCGCGGGAGCCAGGCTTCTGCTGCTGCTGCTGCTGCG 653
QY 114 ProValCyLeuAspArgProIleTYrProCyAspSerLeuCyGluAlaValArgAla 133
DB 654 CCCGCTGCTGTGAGCGCGGCCCATCTACCGCTGTGCTGCTGCTGCGAGCCGTGGCGAC 713
QY 134 GlyCyAlaProLeuMetGluAlaTYrglyPheProTPrProGluMetLeuH1eCyGlnH1 153
DB 714 TCGTGCAGACCGGTATGATGATCTTCGGCTTCTACTGCGCCGAGATGTTAAAGTGTAC 773
QY 154 LysPheProLeuAspAsnAspLeuCyGlnH1eAlaValGlnPheGlyH1s---LeuProAla 172
DB 774 AAGTTCGCG--GAGGGGAGCGTGCATCGCCATGACCGCCGCCCAATGCCAGGAGCC 830
QY 173 ThrAlaProProValThrLysIleCyValAlaGlnCyGluMetGlnH1eSerAlaAspGly 192
DB 831 TTCAGAGCCCAAGGCAACAGGTGTGTCTCCCTGTGACAGAGTGAATCTGAGGCC 890
QY 193 LeuMetGluGlnMetCySerSerSerAspPheValValLysMetArgIleLysGluLys 212
DB 891 ATCATGGAACATCTGTGTGCGAGGTTGCACTGAGAGATGAATAAATAAGAGTGA 950
QY 213 IleGluAsnGlyLysArgLysLeuIleGlyAlaGlnLysLysLysLysLeuLysPro 232
DB 951 AAGGAAATGGCGAGCAAGAAAGATTGTC-----CCCAAGAAAGAGAGCCCTGAGGTG 1004
QY 233 GlyProLeuLysArgLysAspThrLysArgLysValLysMetLysAsnGlyLysGly 252
DB 1005 GGGGCCATCAAGAGAGAGAGCTGAAGAGCTTGTGTCTTACCTAGAGATGGGGTGCAC 1064
QY 253 CySProCySProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyTYrglyVal 272
DB 1065 TGTCTCTGTCACACAGTGTGAGCAACCTCAAGCAACCTTCTCATATGAGCGCGCAAGGTG 1124
QY 273 AspGlyGlnLeuLeuMetAlaValTYrArgTPrAspLysLysLysLysGluMetLys 292
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DB 1125 AAGAGCCGACTTGTCTGACGGCCATCCACAGTGGGCAAGAAACAGAGATTCAA 1184
QY 233 PheAlaValLysPheMetPheSerTYrProCySerLeuTYrTYrPhePhe 310
DB 1185 AACTTCATGAAGAAATGAAAAACATGATGAGGCCACCTTTCAGTGTGTTT 1238

RESULT 2
US-10-821-234-137/c
; Sequence 137, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PE_SEQ_genes Version 1.0
; SEQ ID NO 137
; LENGTH: 4608
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-137

Alignment Scores:
Pred. No.: 8,68e-75 Length: 4608
Score: 916.00 Matches: 179
Percent Similarity: 72.0% Conservative: 50
Best Local Similarity: 56.3% Mismatches: 77
Query Match: 52.9% Indels: 12
DB: 8 Gaps: 7

US-10-768-566-1 (1-317) x US-10-821-234-137 (1-4608)
QY 2 ArgAlaAlaAlaAlaAlaGly-----GlyValArgThrAlaAlaLeuAlaLeu 18
DB 4315 AGAGCCGGCATGGGCGATGGGCGCAGCGAGGGGGCGCGGGGGCGCTGGGGCTGCTG 4256
QY 19 -----LeuGlyAlaLeuH1eTPrAlaProAlaArgCyGluGluLysAspTYTYrgly 36
DB 4255 CTGGGCGTGGGGCGGGCGCTTCTGGCCGTGGGCTGGCCAGGAGTACGACTACGTGAGC 4196
QY 37 TrgAlaAlaGlu-----ProLeuH1s---GlyArgSerTYrSerLysProProGlnCy 53
DB 4195 TTCAGTGGACATCGGCGCCGTACAGAGCGGGCGCTTCTACAGCAGCCAGCTCAGTGC 4136
QY 54 LeuAspIleProAlaAspLeuProLeuCyGlnH1eTPrValGlyTYrLysArgMetArgLeu 73
DB 4135 GTGGACATCCCGCGGACCTGGGGCTGTGCCAGACGTGGGGCTTCAAGAAATGTGCTG 4076
QY 74 ProAsnLeuLeuGluH1eGluSerLeuAlaGluValLysGlnGlnAlaSerSerTPrLeu 93
DB 4075 CCCAAGCTGTGTGAGCAGACAGACCATGTGGGAGGTGAAGCAGACAGCGCGTGGGTG 4016
QY 94 ProLeuLeuAlaLysArgCyGlnH1eSerAspThrGlnValPheLeuCySerLeuPheAla 113
DB 4015 CCCCGCTCAACAGAACTGCGCAGCGCCGAGCCCAAGGCTTCTGCTGCTGCTGCTGCG 3956
QY 114 ProValCyLeuAspArgProIleTYrProCyAspSerLeuCyGluAlaValArgAla 133
DB 3955 CCCGCTCTGTGAGCGCGGCCATCTACCGGTGTGCTGCTGCTGCGAGCGCGTGGCGAC 3896
QY 134 GlyCyAlaProLeuMetGluAlaTYrglyPheProTPrProGluMetLeuH1eCyGlnH1 153
DB 3895 TCGTGCAGACCGGTATGATGATCTTCGGCTTCTACTGCGCCGAGATGTTAAAGTGTAC 3836
QY 154 LysPheProLeuAspAsnAspLeuCyGlnH1eAlaValGlnPheGlyH1s---LeuProAla 172
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Db 3835 AAGTCCCG--GAGGGGAGCTGTGCATGCGCATGAGCCSSCCAAATGCCAGAGCC 3779
 Qy 173 ThrAlaProProValThrlYvllleCyvalaGlnCygluMetGlnHisSerAlaAerGly 192
 Db 3778 TCCAGCCCCCAAGGACAAAGCGGTGTCTCTCCCTGTGACAGACAGATTGAATCTAGAGCC 3719
 Qy 193 LeuMetGlnGlnMetCysSerSerAerPheValValIyMetAerGlyIleYvsluIleYv 212
 Db 3778 ATCATTTGAACATCTGTGTGTCAGCGAGTTTGACAGAGATGAATAATAAAGAGTGA 3659
 Qy 213 lIleGluAerGlyAerPheValIleGlyValaGlnIyValYvsluIleYvsluIleYvPro 232
 Db 3658 AAGGAAATGTGGCAGAGAAAGATGTTC-----CCCAAGAGAGAGAGCCCTTGAAGTTG 3605
 Qy 223 GlyProLeuIyAerGlyAerPheValIleGlyValaGlnIyMetIyAerGlyValaGly 252
 Db 3604 GGGCCCATCAAG 3545
 Qy 253 CysProCysProGlnIleuAerPheValaGlySerPheIleuValMetGlyAerGlyVala 272
 Db 3544 TGTCCCTGCGACAGCTGTGAGCAACCTCAAGCAGCACTTCTCATGATGGCGGAGAGTG 3485
 Qy 273 AserGlyIleuIleuMetAlaValIyAerGlyPheValYvsluIleYvsluIleYv 292
 Db 3484 AAGAGCCAGTACTGTGTGACGGCCATCCCAAGTGGAGAGAGAGAGAGAGAGAGAGAG 3425
 Qy 293 PheAlaValIyPheMetPheSerIyProCysSerIeutyTrTyPhePhe 310
 Db 3424 AACTCATGAG 3371

RESULT 3
 US-11-245-147-197
 ; Sequence 197, Application US/11245147
 ; Publication No. US20060030541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GARCIA, TERESA
 ; APPLICANT: ROMAN ROMAN, SERGIO
 ; APPLICANT: BARON, ROLAND
 ; APPLICANT: CALI, KATHERINE
 ; APPLICANT: THEILHABER, JOACHIM
 ; APPLICANT: CONNOLLY, TIMOTHY
 ; APPLICANT: JACKSON, AMANDA
 ; APPLICANT: BUSHNELL, STEVEN
 ; APPLICANT: RAMADI, GEORGES
 ; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
 ; FILE REFERENCE: 37991-0023
 ; CURRENT APPLICATION NUMBER: US/11/245,147
 ; CURRENT FILING DATE: 2005-10-07
 ; PRIOR APPLICATION NUMBER: PCT/IB02/02211
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,400
 ; PRIOR FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 246
 ; SOFTWARE: Patent In Ver. 3.2
 ; SEQ ID NO 197
 ; LENGTH: 1382
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Homo sapiens secreted frizzled-related protein 2
 ; OTHER INFORMATION: (SFRP2), mRNA.
 US-11-245-147-197

Alignment Scores:
 Pred. No.: 3,34e-48 Length: 1382
 Score: 624.00 Matches: 132
 Percent Similarity: 57.0% Conservative: 51
 Best Local Similarity: 41.1% Mismatches: 97
 Query Match: 36.1% Indels: 41
 DB: 9 Gaps: 7

US-10-768-566-1 (1-317) x US-11-245-147-197 (1-1382)

Qy 5 AlaAlaAlaGlyGlyValaIyGlyPheAlaAlaIleuIleuGlyValaIleuHisTrp 24
 Db 137 GCGGGCCCGGAGCAAGCTGCAAGTCCGGGCGGCTTCCCGGCTCCGCTCCGCTCCGCTCCGCT 196
 Qy 25 AlaProAlaAerGlyGlyIleuIyAerPheValIyMetAerGlyIleYvsluIleYv 36
 Db 197 GCGCCCTGGGGGTGGCGGCGGCGGAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256
 Qy 37 -----TrpGlnAlaGly 40
 Db 257 CCGGCTCCGAGAGCTGCTCCGAGGCTGGGCGGCGGCTTCTCTTCTTGGCCAGCCGCA 316
 Qy 41 ProIleu-HisGlyAerGlyTrpSerIyProProGlnCysIleuAerPheValaAerPhe 60
 Db 317 CTTCTCTCAAG 361
 Qy 60 uProIleuCysHisIyPheValaIyGlyIyAerMetAerGlyProIleuIleuGlnHisGly 80
 Db 362 GAGCTGTGGCAGGAGATGCAATACAGAGATGCGGCTGCGCAAGCTGTGGGCGAGCA 421
 Qy 80 uSerIleuAlaGlyValaIyGlnGlnAlaSerSerTrpIleuProIleuAlaIyAerGly 100
 Db 422 GACCATGAAG 481
 Qy 100 sHisSerAerPheIyGlnValaIleuIyCysSerIeupheAlaProValCys-----Le 117
 Db 482 CCACCGGAGACCAAG 541
 Qy 117 uAerPheProIleuIyTrpProCysAerSerIeupheValaValaIyAerGlyValaAerPhe 137
 Db 542 AGACGAG 601
 Qy 137 OleuMetGlnAlaIyGlyIyPheProIyProGlnIleuIleuIyCysHisIyPheProIle 157
 Db 602 GGTCAATGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTTGTGCGCTT 661
 Qy 157 uAerPheAerPheCysIleuAlaValaIyGlnPheGlyHis-----LeuProAlaAerPhe 173
 Db 662 GAGACAG 721
 Qy 174 -AlaProProValThrlYvllleCyvalaGlnIyMetGlnHisSerAlaAerGly-- 192
 Db 722 AGCTTCA-----AAGTATGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 772
 Qy 193 -LeuMetGlnGlnMetCysSerSerAerPheValValIyMetAerGlyIleYvsluIleYv 212
 Db 773 CATTAATGAG 832
 Qy 212 sIleGluAerGlyAerPheValIleGlyValaGlnIyValYvsluIleYvsluIleYvPhe 232
 Db 833 CTACATCAAG 892
 Qy 232 OGlyProLeuIyAerGlyAerPheValIleGlyValaGlnIyMetIyAerGlyValaGly 252
 Db 893 GAACGCTGTGTCGAG 952
 Qy 252 yCysProCysProGlnIleuAerPheValaGlySerPheIleuValMetGlyAerGlyVala 272
 Db 953 GTGACCTGTGAG 1012
 Qy 272 lAserGlyIleuIleuMetAlaValIyAerGlyPheValYvsluIleYvsluIleYv 292
 Db 1013 GGGTGGGAG 1072

RESULT 4
 US-09-925-065A-678403
 ; Sequence 678403, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:

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1  APPLICANT Wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single
3  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
4  FILE REFERENCE: 108827.135
5  CURRENT APPLICATION NUMBER: US/09/925,065A
6  CURRENT FILING DATE: 2001-08-08
7  PRIOR APPLICATION NUMBER: US 60/243,096
8  PRIOR FILING DATE: 2000-10-24
9  PRIOR APPLICATION NUMBER: US 60/252,147
10 PRIOR FILING DATE: 2000-11-20
11 PRIOR APPLICATION NUMBER: US 60/250,092
12 PRIOR FILING DATE: 2000-11-30
13 PRIOR APPLICATION NUMBER: US 60/261,766
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: US 60/289,846
16 PRIOR FILING DATE: 2001-05-09
17 NUMBER OF SEQ ID NOS: 957086
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO 678403
20
21 LENGTH: 2379
22
23 TYPE: DNA
24
25 ORGANISM: Homo sapiens
26
27 US-09-925-065A-678403

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Alignment Scores:			
Pred. No.:	1,08e-47	Length:	2379
Score:	621.50	Matches:	153
Percent Similarity:	57.0%	Conservative:	17
Best Local Similarity:	51.3%	Mismatches:	75
Query Match:	35.9%	Indels:	54
DB:	6	Gaps:	7
US-10-768-566-1 (1-317) x US-09-925-065A-678403 (1-2379)			
QY	37 TRPGLNlaagluProLeuNHlaGlyAxsSerTySerLeuProProGlnCyLeuAsp-11 56		
Db	253 TGGGAATCAATCCCA---GAGATCAGGAAGTCCACCTCCCTCATCAAGATCCCT 30		
QY	56 eProlaAerLeuProLeuCyNHleThValGlyTyTyLysArgMetArgLeuProAsnLe 76		
Db	310 TCCAAAGAGTCGGCCCCAGTCCCATCCATCCCT-TATCCCTCTCTGGAGGCCACAT 368		
QY	76 uLeuGlnHlaGlnSerLeuHlaGluValuylGlnGlnAlaSerSerTrpLeuProLeuLe 96		
Db	369 GCGCTTCCATCAAGAGCTC-----TCCACCTCGCTTTGGT 404		
QY	96 uAlaLysArgCyNHlSerSerThrGlnValPheLeuCySerLeuPheAlaProValCy 116		
Db	405 G-----TCTCAAGAGGGCTTGAAGCTTGCATTCGATTCAGCCAGGTCAC 444		
QY	116 sLeuAspArgProLeuTyPro-----CyVar 125		
Db	444 AGGCTCTACCCCTCAATCCCTCTGTACCTTGAGATGAAGGTAGTGTGTGCC 503		
QY	125 gSerLeuCyGluAlaValArgAlaGly-----CyAlaProLeuMetGluAl 141		
Db	504 TTGAGAGTGCAGCATGATGAAGTCTTCATTAATATGAATAATGTGCC-----CTACGAGC 557		
QY	141 aTyArgLysPheProTrpProGlnMetLeuNHlSerNHlLysPhePheProLeuAspAsnAspLe 161		
Db	558 TCCACCTTTCCAAAGCCCGAGGGAGCTC----- 585		
QY	161 uCyAlaAlaValGlnPheGlyNHlSerProAlaThrAlaProProValThrLysIleCy 181		
Db	586 -----AGGCTCCCCAGGCCGAAAGTCCAGAAACACCAACATC 622		
QY	181 sAlaGlnCyGluMetGlnHlSerAlaPheGlyLeuMetGlnMetCySerSerAs 201		
Db	624 TGTGCCACACAGGATCCCAACAGATCTACCATTTCCAACTGGCCCTGTCTTTCTTC 683		
QY	201 pPhe-ValValLysMetArgLleLysGlnIleLysIleGlnGlnGlyAspArgLysLeuI 221		
Db	684 CCAACAGTGGTCAAAATGGCATCAAGAGATPAAAGATAGAGATGGGAGCGGAAGCTGA 744		

[illegible]

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RESULT 5
US-11-245-147-5
; Sequence 5, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHAER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAMADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTROGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/I802/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-245-147-5

Alignment Scores:
Pred. No.:      1.29e-47      Length:      926
Score:          615.50       Matches:     126
Percent Similarity: 61.8%    Mismatches: 52
Best Local Similarity: 43.8% Indels:         93
Query Match:     35.6%      Gaps:        17
DB:              9          7

US-10-768-566-1 (1-317) x US-11-245-147-5 (1-926)

QY      13 A|A|A|A|A|A|A|A|A|A|G|U|G|U|A|A|A|U|H|I|S|T|R|P|A|A|P|R|O|L|A|A|A|G|Y|G|U|G|U|Tyr 32
      |||||:::|||:::|||:::|||:::|||
Db      36 GCGTCGCTGTGTGTGTATCTCTGCCTCCGACCGCGTGCGCTCGGGAGCTCGGCGCGTGGAGCTC 95

QY      33 AsP|Ty|Ty|G|U|T|Tp|G|A|A|A|G|U|D|Pro|Leu|H|Se|L|y|A|G|Ser|Ty|r|Ser|Ly|S|Pro|Pro|Gln 52
      ::|||:::|||:::|||:::|||:::|||:::|||
Db      96 TTCCTCTTCGGC---CAGGCCGACTTCTCTCAAGCCAGCCAACTCCAAAGCCC----- 146

QY      53 CyA|Leu|Asp|I|e|r|ro|A|Asp|Leu|Pro|Leu|Cy|H|S|Tr|Val|G|U|T|Ty|A|A|G|Met|Arg 72
      |||||:::|||:::|||:::|||:::|||:::|||:::|||
Db      147 -----ATCCCGCCAACTGCAGCTGTGCCACGGCATCGAGTACGAGTACCAAGACGTGCGG 197

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[illegible]

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Db      1057 GACCATGAAGAGGTGCTGAGCAGCGCCGGCGCTTGATCCCGGTGCATGAAGCAGTG 1116
QY      100  eHiSeRAspRhrtGlnValPheLeuCySeSerLeuPheAlaProValCyS-----Le 117
Db      1117 CCACCCGGACACCAAGAAAGTTCTGTGCTGTCTCTTTCGCCCCCGTCGCTCGATGACT 1176
QY      117  uASpAspProIleTyRProCySaTgSerLeuCySeGluValaValaRgaIaGlyCysAlaPr 137
Db      1177 AGACGACGACCATCCAGCCATTCACCTGCCTTGGGTGCAAGGTGAAGAACCGCTGCCCC 1236
QY      137  oLeuMeGluValaTyRglYpHeProTIRProGluMeLeuHiASyShIaTyRAspProLe 157
Db      1237 GGTATGTCGCGCTTCGCGCTTCCTCCCTGCGCCGACATGCTTGAATGCGCACGCTTCCCCA 1296
QY      157  uASpAspAspLeuCySIIeAlaValaGlnPheGlyHiS-----LeuProAlaThr----- 173
Db      1297 GGACACACGACACTTTCGATCCCTCCCTCGTACGACGACCACTCTCTGCGACGACACCGAGA 1356
QY      174  -----AlaProProValTh 178
Db      1357 AGGTAAAGCTTCCTCTTCTTCTTCCCACTCCCTGCGCTGAGACGCTCCAGAGACTC 1416
QY      178  rLySIIeCyS-----AlaGlnCyS 184
Db      1417 CCGCCCTGCACGACGATCCGACTGC 1441

RESULT 10
US-11-184-005-23
; Sequence 23, Application US/11184005
; Publication No. US20050256052n1
; GENERAL INFORMATION:
; APPLICANT: luyten, Frank P.
; APPLICANT: Moos, Malcom JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
; FILE REFERENCE: NIH133.ICPC3
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: Xenopus laevis
US-11-184-005-23

Alignment Scores:
Pred. No.: 1,16e-16 Length: 1291
Score: 285.00 Matches: 76
Percent Similarity: 46.2% Conservative: 50
Best Local Similarity: 27.8% Mismatches: 93
Query Match: 16.5% Indels: 54
DB: 12 Gaps: 11

US-10-768-566-1 (1-317) x US-11-184-005-23 (1-1291)
QY      57  ProHlaAspLeuProLeuCySHIstHValGlyTyTyRAspRgmMetARgLeuProAsnLeu 76
Db      178  CCGTGGCGAGATCCCATATGCAATCTATGCGATGCAACATGACCAAGCAATGCCAACCAT 237
QY      77  LeuGluHISgluSerLeuAlaGluValaGlyGlnGlnAlaSerSerTIRProLeuProLeu 96
Db      238  CTCACACACAGCACTCAAGCAATGCTATCTCGGCAATTGAACAGTTTGAAGTTTCTGT 297
QY      97  AlAlaTyRAsyCySHISeRAspRhrtGlnValaPheLeuCySeSerLeuPheAlaProValCyS 116

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Db      298 ACCACTGAATGATGACGAGACCTTTTGTCTTCTGTGTGCGCATGTATATCCCATTTGT 357
      117 Leu-----AapArpProIleTyProCyArgSerLeuCyArgLysValaValaArg 132
      358 ACCATCGATTTCCAGATGATGACCAATTAAAGCTTGTGAAGTCCGTGTGCCAAGGGCCAG 417
      133 AAGAGTCyArgAlaProLeuMetGluAlaTyArgLysPheProTyrProGluMetLeuHisCy 152
      418 GCCGGCTGTGAGCCATCTCATTAAGTACCGGCACACTTGGCCAGAGAGCTGGCATGT 477
      153 HisLysPheProLeu---AapAnaPheLeuCyHisAlaValGlnPhe----- 167
      478 GAAGAGCTCCCGTATATGACAGAGAGTGTGATCTCCCGAGAGCTATCTGCACAGTG 537
      168 -----GlyHisLeuPro 171
      538 GAACAAAGAACAGATTCAATGCCAGACTTCCCATGATTCACAAACAATGGAAATGCCGA 597
      172 AATAThAlaProProValThyTyArgLysAlaGlnCyArgLysMetGluHisSerAlaAap 191
      598 AACACGGCA-----GATGACACTGTAAATGCAAGCCCATGAAAGCTTCCCAAG 648
      192 GlyLeuMetGluGlnMetCysSerSerAapPheValValLysMetArgLysGluLe 211
      649 ACGTATCTCAAGAAAT-----AATTCAATTATGATATCAGAGCAAAATGAAAGAGTG 702
      212 LysIleGluAsnGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLysLeuLys 231
      703 AAGGTAAATGCCACGACACGACACGCAATT-----GTGGAAATAAGAGATTTCTCAAG 756
      232 ProGlyProLeuLys---ArgLysAapThyTyArgLysValLeuHisMetLysAsnGly 250
      757 TCTTCCCTAGTAAACATCTCTTAAGACACAGTACACTGTAC-----ACCAAC 804
      251 AAGLysCysProCysArgProGlnLeuAapSerLeuAlaGlySerPheLeuValMetGlyArg 270
      805 TCAGGCTGCTTGTGCCCCCAGCTTGTGTGC---AATGAGAAATACATAATTATGGGCTAT 861
      271 Lys-----ValAspGlyGlnLeu----- 276
      862 GAAGACAAAGAGCGTCCAGGCTTCTAATGAGTGAAGGATCCTTGGCCCAAAATGAGAGA 921
      277 -----LeuLeuMetAlaValTyArgTyrAapLys 287
      922 GATCGCTTGTCTAAAGAAATCAAGCGCTGGATCAAAAG 960

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RESULT 11
 US-11-184-005-1
 / Sequence 1, Application US/11184005
 / Publication No. US20050256052A1
 / GENERAL INFORMATION:
 / APPLICANT: Luyten, Frank P.
 / APPLICANT: Moos, Malcolm JR.
 / APPLICANT: Hoang, Bang
 / APPLICANT: Wang, Shouwen
 / TITLE OF INVENTION: METHOD OF MODULATING TISSUE
 / TITLE OF INVENTION: GROWTH USING FRZB PROTEIN
 / FILE REFERENCE: NIH133_1CPC3
 / CURRENT APPLICATION NUMBER: US/11/184,005
 / CURRENT FILING DATE: 2005-07-18
 / PRIOR APPLICATION NUMBER: US 10/028051
 / PRIOR FILING DATE: 2001-12-19
 / PRIOR APPLICATION NUMBER: US 08/822333
 / PRIOR FILING DATE: 1997-03-20
 / PRIOR APPLICATION NUMBER: US 08/729,452
 / PRIOR FILING DATE: 1996-10-11
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 2374
 / TYPE: DNA
 / ORGANISM: Bos taurus

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US-11-184-005-1
Alignment Scores:
Pred. No.: 3,286-16
Score: 283.50
Percent Similarity: 41.54
Best Local Similarity: 26.14
Query Match: 16.44
DB: 12 Gaps: 11

US-10-768-566-1 (1-317) x US-11-184-005-1 (1-2374)
      2 ArgAlaAlaAlaAlaAlaGly-GlyValArgThrAlaAlaLeuAlaLeuLeuGlyAl 21
      276 CGGAGATGCTGCTGCTGCGCGCGCGGCTACTGCGCTGCGCTGCGCTGCTGCGCTG 335
      21 AlaHisArgAlaProAlaArgCyArgLysGluTyrAspTyrTyArgLysTrpAlaGluPr 41
      336 GCCCGAGCGCGCGCGCGCGCTGTGAG----- 363
      41 AlaHisArgLysSerTyrSerLysProProGlnCysLeuAapLysProAlaAapLeuPr 61
      364 -----CCGTTCCGATTC 377
      61 AlaCysHisArgThyValGlyTyrLysArgMetArgLeuProAnaLeuGluHisGlyLe 81
      378 CCGTGTGCAAGTCCCTGCGCGCTGGACATGATGATGAAGTGCCCAACCACTGTGCACAGAGC 437
      81 rLeuAlaGluValLysGlnGlnAlaSerSerTyrLeuProLeuAlaValArgCysHis 101
      438 CAGAGCAAGCCCATCTCGGCATGACAGAGTTCAAGAGTCTGCTGTGGCACCACCTGCGAG 497
      101 sSerAapThrGlnValPheLeuCysSerLeuPheAlaProValCysLeu----- 117
      498 CCGGATGCTGCTCTTCTCTCTGTGTATGAGCGCCCATCTGCACATGACTTCA 557
      118 -AapArpProIleTyProCysArgSerLeuCyArgLysAlaValaValaGlyCysAlaPr 137
      558 GCACAGCAAGCCCATCAAGCCCTGTGCAAGTCTGTGTGCGAGGGCGCGCGAGGTGTGAGGC 617
      137 AlaMetGluAlaTyArgLysPheProTyrProGluMetLeuHisCysHisLysPheProLe 157
      618 CATCTCATCAAGTACCGGCACTCGTGTGCGGAAAGCTTGAGCTGTGAGAGAGCTGCAGT 677
      157 u---AapAnaPheLeuCyValAlaValaGlnPheGlyHisLeuProAlaThrAlaProPr 176
      678 ATATGACCGCGCGCGGTGATCTGTCCGAG-----GCCAT 713
      176 oValThyTyArgLysCysValaGlnCysGluMetGluHisSer-----AlaAapGlyLe 193
      714 CGTCACTGCCGACGAGCGGATTTTCTATGATTCAGTATGGAACCTGTAGAGGAGC 773
      193 uMetGluGlnMetCys----- 198
      774 AAGCAGTGAACGCTCAAAATGTAACCAAGTCAAGACTACACAGAAACCTATTTCGAAA 833
      199 -sSerAapPheValValaLysMetArgLysGluLeuLysIleGluAsnGlyAspAr 218
      834 CAATTAAACAATATGATTCATTCGGCGGTAAAGTTAAATAAAGAACCAAGTGCATGAT-- 891
      218 GlyLysLeuIleGlyAlaGlnLysLysLysLysLeuLeuLysProGlyProLeuLysArgLys 238
      892 ---GTGACTGAGTGTGAGAGGTGAAGAGATTTTAAAGCTTCTCTGTGTA----- 939
      238 AlaPheThyTyArgLysValLeuHisMetLysAsnGlyAlaGlyCysProCysProGlnLe 258
      940 -AACATTCCAAGGAAAGTGTGAACCTTATACCAAGCTGTGCTGTGTGCTTCCACT 998
      258 uAapSerLeuAlaGlySerPheLeuValMetGlyTyArgLys----- 271
      999 T---AAGCTTATGAGAGTATCTATCATCATGCGGTACGAAGTGAAGAGCGCTCAAGATT 1055
      272 -----ValAapGlyGlnLeu-----LeuLeuMetAlaValTy 282

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Db      1056 ACTGTGGTACGAAGCTTTATTTCCTGCAAGAAATGGAAGATGCACCTTGGTAAATAAGTTAA 1115
Qy      282 TArgTTPaPlySLySaenLySgUmeC 291
Db      1116 GCGGTGGATATGAAGCTCCGATCCTT 1143

RESULT 12
US-11-054-281-35
; Sequence 35, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; -PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-054-281-35

Alignment Scores:
Pred. No.:      6,31e-16      Length:      2184
Score:          280.00      Matches:      68
Best Similarity: 50.6%      Conservative: 22
Best Local Similarity: 38.2% Mismatches:      64
Query Match:    16.2%      Indels:        26
DB:             12          Gaps:           6

US-10-768-566-1 (1-317) x US-11-054-281-35 (1-2184)
Qy      5 AAlaAlaIaGIyGLyValArgThraAlaLeuAlaLeuLeuGLyAlaLeuHisTrp 24
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      37 GCCTTGGCGGGGGGCGCTGCTGTGTGCAAGCTGCTGG-CGGCGGGCGGGCGGCACCTGG 95
Qy      25 AAlaProAlaArgCySgLUgluLutyrAspTyrTyrgLutyrGlnAlaGluProLeuHisGLy 44
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      96 AGATC-GGCGCG-----TTGCAACCGGAGGCGCGG 124
Qy      45 ArgSerTyrSerLysProProGlnCysLeuAspLleProAlaAspLeuProLeuCysHis 64
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      125 CGCGGG--GCTGCCCGCTGCCAGCGCGGTGGAGATC-----CCCATGTGCCGC 169
Qy      65 ThrValGLyTyrLysArgMetArgLeuProAsnLeuGluHisGLuSerLeuAlaGlu 84
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      170 GGCATCGGCTTACACTTGAACCCGCAATGCCCACTTCTGGGGCCACAGTCCGAGGCGAG 229
Qy      85 VallySgInGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCysHisSerAspThr 104
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      230 GCGGCTGCCAGACTGACGGAAGTTCGCGCGCGTGGTGCAGTACCGGTGCCACAGCACTGT 289
Qy      105 GlnValPheLeuCysSerLeuPheAlaProValCysValAspArg-----ProIle 121
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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Db      290 CGGTTCTTCTCTGTCGCTCGCTTACGGCGCCCATGTGACACCGACCGACGAGTCTCGACGCCCAT 349
Oy      122 TyPProCyatgSerLeuCyGsluaValAAlgaaglyCyvalaPProLeuMetGslua 141
Db      350 CCGCGCTCGCGCCCATGTGACGACGAGCGCGCTGCGCGCTCGCGCCCATCATGAGACAG 409
Oy      142 TyGlyPheProTProProbiLumetLeuHiaCySHisLysPheProLeuAaPaaAaP 160
Db      410 TTCACCTTGCGCGTGGCGGAGATCGCTGCACATGCGCGCGGAGCTGGCCACGCGCAGACCG 469
Oy      161 -----LeuCyGslleaValGlnPheGlyHisLeuProAlaThrAlaProPro 176
Db      470 CACGCGCTGTGATGAGCGCGCGCGCAGAAC-----GCCACGCGCGCGCC 514

RESULT 13
US-11-184-005-3
; Sequence 3, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; TITLE OF INVENTION: GROWTH USING PZB PROTEIN
; FILE REFERENCE: NIH133.1CPC3
; CURRENT APPLICATION NUMBER: US/11/194,005
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-184-005-3

Alignment Scores:
Pred. No.: 4,46e-16 Length: 1484
Score: 279.50 Matches: 85
Percent Similarity: 41.5% Conservative: 52
Best Local Similarity: 25.8% Mismatches: 113
Query Match: 16.2% Indels: 80
Db: 12 Gaps: 11

US-10-768-566-1 (1-317) x US-11-184-005-3 (1-1484)
Oy      2 ArgAlaAlaAlaAlaAlaGly-GlyValAlxThraAlaAlaLeuAlaLeuLeuGlyAl 21
Db      228 AGGAGATGCTGCTGCTGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGGAT 287
Oy      21 aleuHiaTProAlaProAlaArgCyGsluglntuTaaPryTyrGlyTyrGlnAlaGlnP 41
Db      288 GCCCGCGGCGCTCGCGGCGCGACGCTGTGAG----- 315
Oy      41 oleuHiaGlyAArgSerTyrSerLysProProGlnCysLeuAaPrlleProAlaAaPrl 61
Db      316 -----CCCGTCCGACATCCC 329
Oy      61 oleuCySHisThrValGlyTyrLysArgMetArgLeuProAaHleuLeuGlnHiaGlySe 81
Db      330 CCTGTGCAAGTCCCTGCTGCTGGAACAATGATTAAGATGCGCAACACCTGCGACACAGAC 389
Oy      81 rleuAlaGluValLysGlnGlnAlaSerSerTyrLeuProLeuLeuAlaLysArgCysH 101
Db      390 TCAAGGCCAAGCGCATCTTGCGCATGAGACAGTGAAGAGTGTGTGGGACCCACACTGCA 449
Oy      101 sSeAaPrrTnGlnValPheLeuCySeSerLeuPheAlaProValCysLeu----- 117

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Db 450 CCCCGATTCGCTCTTCTTCTCTGTCAGTACGGCCCATCTGACCATTCGACTTCCA 509
Qy 118 -AsparGProIeTyPrOCyArGSeRSeuCyGuaIaValArGAlaGlyCyAlaPr 137
Db 510 GCACGAGCCCATCAAGCCCTGTAGTCTGTCTGCGAGCGGCGCCGACAGGCTGTAGCC 569
Qy 137 oLeuMeTGuAlaTyGlyPheProTrProGluMeTLeuHiSeRSeuCyHiLyPheProLe 157
Db 570 CATCTCATCACTACAGTACCGCCACTCGTGGCCGAGAACCTGGCCTGCGAGAGCTGCCAGT 629
Qy 157 u---AspaNaBrLeuCyeTleAlaValaGlnPheGlyHiLeuProAlaThrAlaProPr 176
Db 630 GTACGACAGGGCGGTGTGCACTCTCCCGAG-----GCCAT 665
Qy 176 oValThrLyIleCyAlaGlnCySeGluMeTGuHiSeR-----AlaAspLyLe 193
Db 666 CGTTATCGGGAGACGAGAGCTGATTTCTCTATGATTTCTAGTAAGAAAGTGTAGAGGGCG 725
Qy 193 uMeTGuIuMeTyS----- 198
Db 726 AAGCACTGAACGCTGTAAATGTAGCCCTATTAGAGCTACACAGAAAGCTATTCCGGA 785
Qy 199 -SeRSeArpPheValValLyMeTArGlyLeuGlyuIleLyIleGluAsnGlyAspAr 218
Db 786 CAATTACAACTATGCTATTCGGGCTAAAGTTAAAGATTAAGACTTAAGTCCATGAT-- 843
Qy 218 gLySeuIleGlyAlaGlnLySeuLySeuLySeuLySeuLySeuLySeuLySeuLySeuLy 238
Db 844 ----GTGACTGCGAGTGTAGAGGTGAAGAGATTCTTAAGTCTCTCTGTGTA----- 891
Qy 238 sArPThrLyArGLeuValLeuHiMeTLeuSaSnGlyAlaGlyCyArProCyArProGluLe 258
Db 892 -AACATTCACAGCGGACACTGTCAACCTCTATACAGCTGTGCTGCTGCTGCTGCTGCTGCT 950
Qy 258 uArSeRSeuAlaGlySeRSeuValMeTGuIaGlyS----- 271
Db 951 T---AAVTGTAATGAGAAATATATCATGAGGCTATGAAGATGAGAAAGTTCAGATT 1007
Qy 272 -----ValAspGlyGlnLeu-----LeuLeuMeTAlaValTy 282
Db 1008 ACTCTTGCTGAGAGGCTCTATAGCTGAGAAGTGAAGATCGACTGGTAAAAAAGTTAA 1067
Qy 282 rArGTrArPArLyLyAsnLySeGluMeT 291
Db 1068 GCGCTGGATATGAGCTTCGTATCTT 1095

RESULT 14
US-11-127-877-26
/ Sequence 26, Application US/11127877
/ Publication No. US20050287565A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spitznagel, Koehnrad F. F.
/ APPLICANT: Laenen, Wendy
/ TITLE OF INVENTION: Method, Compositions and Compound Assays For Inhibiting
/ TITLE OF INVENTION: Amyloid-beta Protein Production
/ FILE REFERENCE: P27, 800-B USA
/ CURRENT APPLICATION NUMBER: US/11/127, 877
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: 60/570,352
/ PRIOR FILING DATE: 2004-05-12
/ PRIOR APPLICATION NUMBER: 60/603,948
/ PRIOR FILING DATE: 2004-08-24
/ NUMBER OF SEQ ID NOS: 590
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26
/ LENGTH: 2561
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-127-877-26
```

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Alignment Scores:
Pred. No.: 1,79e-15 Length: 2561
Score: 276.00 Matches: 62
Percent Similarity: 52.14 Conservative: 25
Best Local Similarity: 37.14 Mismatches: 64
Query Match: 16.04 Indels: 16
DB: 12 Gaps: 6

US-10-768-566-1 (1-317) x US-11-127-877-26 (1-2561)
Qy 19 LeuGlyAlaLeuHiSeRValAlaProAlaArCySeGluGluTyArPTrTyGlyTrGln 38
Db 390 CTGGCTGACCCATCCGCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
Qy 39 AlagluProLeuHiSeRValAlaProAlaArCySeGluGluTyArPTrTyGlyTrGln 58
Db 450 GCC-----GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 493
Qy 58 lArPLeuProLeuCySeHiSeRValAlaGlyTyTrLyArGMeTArGLeuProAlaLeuG 78
Db 494 --ACGGTCCCATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 551
Qy 78 lUHiGluSeRSeuAlaGluValLyGlnGlnAlaSeRSeRTrPLeuProLeuAlaL 98
Db 552 ACCACGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 611
Qy 98 yArGCySeHiSeRArPThrGlnValPheLeuCySeRSeuPheAlaProValCySeu- 117
Db 612 TCCATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 671
Qy 118 -----AspArGProIeTyPrOCyArGSeRSeuCyGuaIaValArGAlaGlyC 135
Db 672 CCGACTACCAACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 731
Qy 135 yAlaProLeuMeTGuAlaTyGlyPheProTrProGluMeTLeuHiSeRSeuLySeu 155
Db 732 GCTGCGCGCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 791
Qy 155 hePro---LeuArPArPArP-----LeuCyAlaAlaValaGlnPheGlyHiSeuP 171
Db 792 TCCCGGTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 848
Qy 171 rAlaThrAlaProPro 176
Db 849 CCACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 865

RESULT 15
US-11-067-231-154
/ Sequence 154, Application US/11067231
/ Publication No. US20050272063A1
/ GENERAL INFORMATION:
/ APPLICANT: Nakamura, Yusuke
/ APPLICANT: Katagiri, Toyomasa
/ APPLICANT: Fukukawa, Chikako
/ TITLE OF INVENTION: METHOD FOR TREATING SYNOVIAL SARCOMA
/ FILE REFERENCE: 1254-0272PUS1
/ CURRENT APPLICATION NUMBER: US/11/067,231
/ PRIOR FILING DATE: 2005-02-28
/ PRIOR APPLICATION NUMBER: US 60/407,506
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/486,195
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/JP03/10591
/ PRIOR FILING DATE: 2003-08-21
/ PRIOR APPLICATION NUMBER: PCT/JP2004/002144
/ PRIOR FILING DATE: 2004-02-24
/ PRIOR APPLICATION NUMBER: US 60/598,834
/ PRIOR FILING DATE: 2004-08-05
/ NUMBER OF SEQ ID NOS: 218
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 154
/ LENGTH: 2811
/ TYPE: DNA
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ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (18) .. (1763)
 US-11-067-231-154

Alignment Scores:

Pred. No.:	8,98e-15	Length:	2811
Score:	269.00	Matches:	66
Percent Similarity:	44.6%	Conservative:	29
Best Local Similarity:	31.0%	Mismatches:	67
Query Match:	15.5%	Indels:	52
DB:	12	Gaps:	7

US-10-768-566-1 (1-317) x US-11-067-231-154 (1-2811)

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QY      57  ProAlaAspLeuProLeuCySHisThrValGlyTyrLeuArgMetArgLeuProAsnLeu 76
      |||  :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      123  CCCATCGAGATCCCGATGTCAGACAGACATCGGCTACACATGACTGTATGCCCAACTG 182

QY      77  LeuGluHisGluSerLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeu 96
      ::|  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      183  ATGGGCCACAGAACCGCGGAGGAGGAGCCATCCATGGACAGATTCCGCGCTGGTG 242

QY      97  AlaLysArgCysHisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCys 116
      |||  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      243  GAGTACGGGTGCCACCGCCACTCCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 302

QY      117  LeuAspArg-----ProIleTyrProCysArgSerLeuGluAlaValArgAla 133
      :::::  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      303  ACCGACGACAGTCTTACCCCGCCACTCCGCGGTCTCATGTGCGAGCGCGCCGCTC 362

QY      134  GlyCysAlaProLeuMetGluAlaTyrGlyPheProTyrProGluMetLeuHisCysHis 153
      |||  :::::|||||:::|||||:::|||||:::|||||:::|||||
DB      363  AAGTGTCTCCCGATTATGAGCAGTTCACACTTCAAGTGCGCCGACTCCTTGACTGCCG 422

QY      154  LysPheProLeuAspAsnAsp-----LeuCysIleAlaValGln----- 166
      |||  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      423  AAACCTCCCAACAAAGAACGACCCCACTACTGTGCATGAGGAGGCCCAACACGGCTCG 482

QY      167  -----PheGlyHisLeuProAlaThrAlaProProValThrLysIle 180
      |||  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      483  GACGACCCGACCCGCGGCTCGGCGCTGTTCCCGCTGTTCCGCGCGACGCGCCAC 542

QY      181  CysAlaGlnCysGluMetGluHisSerAlaAspGlyLeuMetGluGlnMetCysSerSer 200
      |||  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      543  AGCGCGCAG-----GAGCAGCC-GCTGAAGGA----- 568

QY      201  AspPheValValLysMetArgIleLysGluIleLysIleGluAsnGlyAspArgLysLeu 220
      |||  |||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      569  -----CGGGGGCCCCCG----- 580

QY      221  IleGlyAlaGlnLysLysLysLysLeuLeuLysProGlyProLeuLysArgLysAspThr 240
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DB      581  -----GCGCGCGCGCTGCGACAAACCGCGGCAAGTTCACCACTGAGAA 625

QY      241  LysArgLeuVal-----LeuHisMetLysAsnGly 250
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DB      626  GAGCGCGCTGCTGCGCGCGCTGCTGCAAGCGCGCGCTGGA 664
  
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Search completed: March 23, 2006, 08:26:16
 Job time : 395 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 22:42:32 ; Search time 47 Seconds
(without alignments)
557.621 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730

Sequence: 1 MRAAAAGCVRTAALALILG.....MFSYPCSLYPPFYGAEPH 317

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	317	2	US-08-937-067-6 Sequence 6, Appli
2	1730	100.0	317	2	US-09-949-016-6300 Sequence 6300, Ap
3	1674	96.8	305	2	US-09-949-016-7706 Sequence 7706, Ap
4	924.5	53.4	314	2	US-08-937-067-7 Sequence 7, Appli
5	917	53.0	313	2	US-09-546-043-3 Sequence 3, Appli
6	917	53.0	338	2	US-09-546-043-4 Sequence 4, Appli
7	915	52.9	313	2	US-09-514-885-1 Sequence 1, Appli
8	915	52.9	313	2	US-09-949-016-6299 Sequence 6299, Ap
9	869.5	50.3	314	2	US-09-087-031E-3 Sequence 1, Appli
10	860	49.7	313	2	US-09-087-031E-4 Sequence 4, Appli
11	714	41.3	267	2	US-09-546-043-7 Sequence 7, Appli
12	659	38.1	246	2	US-09-546-043-6 Sequence 6, Appli
13	617.5	35.7	295	2	US-08-937-067-2 Sequence 2, Appli
14	610.5	35.3	295	2	US-09-999-833A-415 Sequence 415, App
15	610.5	35.3	295	2	US-10-020-445A-415 Sequence 415, App
16	609	35.2	295	2	US-09-148-545-179 Sequence 179, App
17	609	35.2	295	2	US-09-621-011-179 Sequence 179, App
18	609	35.2	296	2	US-09-148-545-237 Sequence 237, App
19	609	35.2	296	2	US-09-621-011-237 Sequence 237, App
20	564.5	32.6	295	2	US-08-893-654B-6 Sequence 6, Appli
21	555.5	32.1	195	2	US-09-546-043-5 Sequence 5, Appli
22	475.5	27.5	212	2	US-08-937-067-4 Sequence 4, Appli
23	442.5	25.6	109	2	US-09-087-031E-19 Sequence 19, Appli
24	401.5	23.0	229	2	US-09-546-043-8 Sequence 8, Appli
25	398	23.0	280	2	US-08-893-654B-4 Sequence 4, Appli
26	381.5	22.1	113	2	US-09-087-031E-24 Sequence 24, Appli
27	372.5	21.5	281	2	US-08-893-654B-2 Sequence 2, Appli

28	285	16.5	319	2	US-10-028-051A-7 Sequence 7, Appli
29	284.5	16.4	572	2	US-08-937-067-13 Sequence 13, Appli
30	283.5	16.4	318	2	US-08-878-474-3 Sequence 3, Appli
31	283	16.4	319	2	US-10-014-055-7 Sequence 7, Appli
32	279	16.1	318	2	US-10-014-055-8 Sequence 8, Appli
33	279	16.1	325	2	US-10-014-055-2 Sequence 2, Appli
34	276.5	16.1	325	2	US-10-028-051A-2 Sequence 2, Appli
35	276.5	16.0	319	2	US-10-028-051A-8 Sequence 8, Appli
36	275	15.9	325	2	US-08-878-474-9 Sequence 9, Appli
37	275	15.9	325	2	US-09-976-594-479 Sequence 479, App
38	275	15.9	325	2	US-10-014-055-4 Sequence 4, Appli
39	275	15.9	325	2	US-10-028-051A-4 Sequence 4, Appli
40	275	15.9	371	2	US-09-949-016-7544 Sequence 7544, Ap
41	272	15.7	323	2	US-08-878-474-7 Sequence 7, Appli
42	270	15.6	585	2	US-08-937-067-9 Sequence 9, Appli
43	263.5	15.2	685	2	US-08-937-067-14 Sequence 14, Appli
44	262.5	15.2	565	2	US-08-937-067-8 Sequence 8, Appli
45	252.5	14.6	111	2	US-10-014-055-6 Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-08-937-067-6
; Sequence 6, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuel
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: ADIPOCTIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-937-067-6
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Query Match 100.0%; Score 1730; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.3e-193;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAAAAGCVRTAALALILGALHWAPACEYDYGGQAEPLHGRSVSKPPQCLIDPDL 60
DB 1 MRAAAAGCVRTAALALILGALHWAPACEYDYGGQAEPLHGRSVSKPPQCLIDPDL 60
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QY 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
QY 121 IYPCSLCEAVYAGACAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKI 180
DB 121 IYPCSLCEAVYAGACAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKI 180
QY 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
DB 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMS 300
DB 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 2

US-09-949-016-6300
Sequence 6300, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,766
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6300
LENGTH: 317
TYPE: PRT
ORGANISM: Human
US-09-949-016-6300

Query Match 100.0%; Score 1730; DB 2; Length 317;

Best Local Similarity 100.0%; Pred. No. 3.3e-193; Mismatches 0; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAAAGGVRATAALALLGALHMAPRCEEDYDYGQAEPLHGRSYKRPQCLDIPADL 60
DB 1 MRAAAAAGGVRATAALALLGALHMAPRCEEDYDYGQAEPLHGRSYKRPQCLDIPADL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRP 120
QY 121 IYPCSLCEAVYAGACAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKI 180
DB 121 IYPCSLCEAVYAGACAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKI 180
QY 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
DB 181 CAOCMEHSADGLMEOWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMS 300
DB 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 3

US-09-949-016-7706
Sequence 7706, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,766
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7706
LENGTH: 305
TYPE: PRT
ORGANISM: Human
US-09-949-016-7706

Query Match 96.8%; Score 1674; DB 2; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.1e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AALALLGALHMAPRCEEDYDYGQAEPLHGRSYKRPQCLDIPADLPLCHTVGYKRM 72
DB 1 AALALLGALHMAPRCEEDYDYGQAEPLHGRSYKRPQCLDIPADLPLCHTVGYKRM 72
QY 73 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRIPYCRSLCEAVR 132
DB 73 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRIPYCRSLCEAVR 132
QY 61 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRIPYCRSLCEAVR 120
DB 61 LPNLEHESLAEVYQOASSWLPILAKRCHSDTOVFLCSLFAVYCLDRIPYCRSLCEAVR 120
QY 133 AGCAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 192
DB 133 AGCAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 192
QY 121 AGCAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 180
DB 121 AGCAPLMEAYGFPMPPEMLHCHKRPDLNDLCIAVOFGHLPTATAPVTKICAOCMEHSADG 180
QY 193 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYKRLVLMKNGAG 252
DB 193 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYKRLVLMKNGAG 252
QY 181 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYKRLVLMKNGAG 240
DB 181 LMEQWCSSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYKRLVLMKNGAG 240
QY 253 CPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMSYPCSLYYPFFYG 312
DB 253 CPCPQDLSLAGSFLVMGRKYDGOQLLMAVYRMDKXKMKFAVKFMSYPCSLYYPFFYG 312
QY 313 AAEPH 317
DB 313 AAEPH 317

RESULT 4

US-08-937-067-7

Sequence 7, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umaneky, Samuel

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

```

; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-937-067-7

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Query Match          53.4%; Score 924.5; DB 2; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.8e-99;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

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QY 1 MRAAAGGVTAAALAL--LGLHMAPARCEEDYGYQAE--PLH-GRSYSKPQCLD 55
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DB 1 MGIHSGEGRGALGVLLALGALLAVGASAEYDVVSQSDIGPQSRFTKPPQCD 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 56 IPADLPCHTGVYKRMRLPNLHESLAIVKQOASSWPLAKRCHSDTOVFLCSIFAV 115
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IPADRLCHNAGVKKKVLNLEHETMAEVKQOASSWVPLNKNCHAGTOVFLCSIFAV 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 116 CDRPIYPCRSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVOFGH--LPATA 174
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 CDRPIYPCRWLCEAVRDCSEFVMOFGFYWPEMLKCDKFP--EGDVCIAMTPPNTEASK 179
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 175 PVTYKICAOCEMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLGAQKKKLLKPGP 234
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 180 PGCTTCPCPCDNEIKSEALIEHLCSBEFLRMKIKKVKENGDKKIV--PKKKKPLKGP 237
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 235 LKRKDTKRLVLMKKNAGCPCPOLDSLASFVLMGKRYDGOILLMAVYRMDKKNKEMKTA 294
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 238 IKKKDLKKLVLYLKNAGDCPCQDLNLSHFLIMGRKVKVSQYLLTAIHKMDKKNKKEPKNF 297
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 295 VKFMFSYPCSLYYPPF 310
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 298 MKKMKNHCEPTFQSVF 313
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RESULT 5
; US-09-546-043-3
; Sequence 3, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffery et al.,
; TITLE OF INVENTION: SECRETED FRIZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-546-043-3

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Query Match          53.0%; Score 917; DB 2; Length 313;
Best Local Similarity 57.9%; Pred. No. 2.8e-98;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

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QY 8 GGVTAALALILGALHMAPAR--CEEYDYGYQAE--PLH-GRSYSKPQCLDIPADLP 62
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DB 8 GGRRAALGVLL--ALGGASGRGLGSEYDVVSFQSDIGPQSRFTKPPQCDVIPADRL 66
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 CHTVGYKRMRLPNLHESLAIVKQOASSWPLAKRCHSDTOVFLCSIFAPVCLDRPIY 122
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 CHNVGYKKMVLNLEHETMAEVKQOASSWVPLNKNCHAGTOVFLCSIFAPVCLDRPIY 126
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 123 PCRSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVOFGH--LPATA PVTYKIC 181
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 127 PCRWLCEAVRDCSEFVMOFGFYWPEMLKCDKFP--EGDVCIAMTPPNTEASKPGCTTVC 185
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 182 AOCMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLGAQKKKLLKGPRLKRTK 241
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 186 PCPDNELKSEALIEHLCSBEFLRMKIKKVKENGDKKIV--PKKKKPLKGLPIKKDLK 243
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 242 RLVIHMKKNAGCPCPOLDSLASFVLMGKRYDGOILLMAVYRMDKKNKEMKFAVFMFSY 301
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 KLVLYLKNAGDCPCQDLNLSHFLIMGRKVKVSQYLLTAIHKMDKKNKKEPKMKMKNH 303
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 302 PCSLYYPPF 310
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 304 ECPFTQSVF 312
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RESULT 6
; US-09-546-043-4
; Sequence 4, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffery et al.,
; TITLE OF INVENTION: SECRETED FRIZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-546-043-4

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Query Match          53.0%; Score 917; DB 2; Length 338;
Best Local Similarity 57.9%; Pred. No. 3.2e-98;
Matches 179; Conservative 50; Mismatches 70; Indels 10; Gaps 7;

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QY 8 GGVTAALALILGALHMAPAR--CEEYDYGYQAE--PLH-GRSYSKPQCLDIPADLP 62
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DB 8 GGRRAALGVLL--ALGGASGRGLGSEYDVVSFQSDIGPQSRFTKPPQCDVIPADRL 66
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QY 63 CHTVGYKRMRLPNLHESLAIVKQOASSWPLAKRCHSDTOVFLCSIFAPVCLDRPIY 122
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DB 67 CHNVGYKKMVLNLEHETMAEVKQOASSWVPLNKNCHAGTOVFLCSIFAPVCLDRPIY 126
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QY 123 PCRSICEAVRAGCAPLMEAYGFPWPEMLHCHFPDLNDLCTIAVOFGH--LPATA PVTYKIC 181
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DB 127 PCRWLCEAVRDCSEFVMOFGFYWPEMLKCDKFP--EGDVCIAMTPPNTEASKPGCTTVC 185
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QY 182 AOCMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLGAQKKKLLKGPRLKRTK 241
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DB 186 PCPDNELKSEALIEHLCSBEFLRMKIKKVKENGDKKIV--PKKKKPLKGLPIKKDLK 243
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QY 242 RLVIHMKKNAGCPCPOLDSLASFVLMGKRYDGOILLMAVYRMDKKNKEMKFAVFMFSY 301
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DB 244 KLVLYLKNAGDCPCQDLNLSHFLIMGRKVKVSQYLLTAIHKMDKKNKKEPKMKMKNH 303
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QY 302 PCSLYYPPF 310
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Db 121 CUDRPIYPCRMICEAVRDSCEPVMGFFGFYPMELKCDKFP--EGDVCIAMTPPNATEASK 179
Qy 175 PAVTKICAOCMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLKP 234
Db 180 PGTTVCPCPDNLKSEBAIIENHCASEFALRMKIKEYKKNKGDKIV--PKKKKPLKGP 237
Qy 235 LRRKDTKRLVLMKNGAGCPCPOLDSLGSFLVMGKRVGDQGLLMAVYRMDKKKMKKA 294
Db 238 IKKDKLKKLVLYLKNAGDCPCGHDNLSHHFLIMGRKRVSGYLLTAHMKMDKKKKEPKNF 297
Qy 295 VKEMFSIPCSLYYPPF 310
Db 298 MKMKNHCEPTFGSVF 313

RESULT 10
US-09-087-031E-4
; Sequence 4, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-4

Query Match 49.7%; Score 860; DB 2; Length 313;
Best Local Similarity 54.3%; Pred. No. 1.3e-91;
Matches 171; Conservative 48; Mismatches 88; Indels 8; Gaps 6;
Qy 1 MRAAAAAGCTA-ATALLGALHMAPRCEYDY--YGMQAEPL-HGRSYSKPQCUDI 56
Db 1 MGIAGSEGRKGLVLLALGALLAVGSASEIDYVSFGSDIGFYSGGFYTKPPCCVDI 60
Qy 57 PADLPLCHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPC 116
Db 61 PADLRLCHNVGYKQVLPNLLHEHETMAEVKQASSWVPLLNKCHAGTGVFLCSLFAVPC 120
Qy 117 LRPPIYPCSLCEAVAGAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGH-LPATAP 175
Db 121 LDRPIYPCRMICEAVRDSCEPVMGFFGFYPMELKCDKFP--EGDVCIAMTPPNATEASK 179
Qy 176 PVTKICAOCMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLKP 235
Db 180 PGTTVCPCPDNLKSEBAIIENHCASEFALRMKIKEYKKNKGDKIV--PKKKKPLKGP 237
Qy 236 KRRDTRKRLVLMKNGAGCPCPOLDSLGSFLVMGKRVGDQGLLMAVYRMDKKKMKKA 295
Db 238 IKKDKLKKLVLYLKNAGDCPCGHDNLSHHFLIMGRKRVSGYLLTAHMKMDKKKKEPKNF 297
Qy 295 VKEMFSIPCSLYYPPF 310
Db 298 MKMKNHCEPTFGSVF 312

RESULT 11
US-09-546-043-7
; Sequence 7, Application US/09546043
; Patent No. 6600018

; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.,
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-7

Query Match 41.3%; Score 714; DB 2; Length 267;
Best Local Similarity 58.4%; Pred. No. 1.1e-74;
Matches 142; Conservative 38; Mismatches 53; Indels 10; Gaps 7;
Qy 8 GGVRTAALLLGLHMAPR--CEEYDYGMQAE--PLH-GRSYSKPQCUDIADLPL 62
Db 8 GGRGALLGVLL-ALGASGRGLSEYDYVSFGSDIGFYSGGFYTKPPCCVDIADLRL 66
Qy 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPCIDRPIY 122
Db 67 CHNVGYKQVLPNLLHEHETMAEVKQASSWVPLLNKCHAGTGVFLCSLFAVPCIDRPIY 126
Qy 123 PCSRICEAVRAGCALMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGH-LPATAPVTKIC 181
Db 127 PCRMICEAVRDSCEPVMGFFGFYPMELKCDKFP--EGDVCIAMTPPNATEASKPGQTYVC 185
Qy 182 AQCEMEHSHADGLMEQSSDFVVKRIKEIKIENGDRKLIQAOKKKLKPPLKRDTK 241
Db 186 PCDNELKSEBAIIENHCASEFALRMKIKEYKKNKGDKIV--PKKKKPLKGPICKKQDQ 243
Qy 242 RLIV 244
Db 244 AYV 246

RESULT 12
US-09-546-043-6
; Sequence 6, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.,
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-6

Query Match 38.1%; Score 659; DB 2; Length 246;
Best Local Similarity 57.6%; Pred. No. 2.7e-68;
Matches 132; Conservative 36; Mismatches 49; Indels 12; Gaps 7;
Qy 8 GGVRTAALLLGLHMAPR--CEEYDYGMQAE--PLH-GRSYSKPQCUDIADLPL 62
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Qy 63 CHTVGYKRMRLPNLLEHESLAEVKQOASSWPLAKRCHSDTOVFLCSLFAVPCIDRPIY 122
Db 67 CHNVGYKQVLPNLLHEHETMAEVKQASSWVPLLNKCHAGTGVFLCSLFAVPCIDRPIY 126
Qy 123 PCSRICEAVRAGCALMEAYGFPWPEMLHCHKFPLDNDLCIAVOFGH-LPATAPVTKIC 181

PRIOR FILING DATE: 1998-03-27
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 PRIOR APPLICATION NUMBER: 60/085323
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 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 35.3%; Score 610.5; DB 2; Length 295;
 Best Local Similarity 43.6%; Pred. No. 1,6e-62;
 Matches 125; Conservative 50; Mismatches 95; Indels 17; Gaps 7

14 ALALLLALHWPAPCEBYUYGMOAEPHLHGRSXSPPCCLDIPADLPCHTVGYKRMRL 73
 7 SLILFLASHCCCLGASAGLFLPG-QDPSYKSNCRP-----IPVLIOLCHGEIYQWML 60
 74 PNLLEHESLAEVYQOASWILPLIAKRCCHSDTOVFLCSLPAPVC--LDRPIYPCSLCEA 130
 61 PNLGHETKKEVLEQADAWIPLVKQCHPDTKKFLCSLPAPVCLDLDLDETIOPCSHLCVQ 120
 QY 131 VRAGCAFLMEAYGPRPEMHLCHKFLPDNDLCTAVQGR--LPAT--APPVTKICAGCEM 186
 DB 121 VKDRCAVPMGAPGPPWDMLECRFPQDNDLCTPLASSDHLTPATEAP--KVCAGCKN 177

Qy 187 EHSADG-1MEONCSSDPVVKRIKEIKIENGDRKLIQAOKKKKLIKPGELKRRKDTKRLVL 245
Db 178 KNUDDNDIMETLCKNDPALKIKYKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVL 237
Qy 246 HMKNAGCPRCPODLSLAGFLYMKRKVDCQQLMLMVYRKDKNKEMK 292
Db 238 WIKDSLQCTCEEMNDINAPYLVWGQKGGELVITSVKRWQKQREPK 284

RESULT 15
US-10-020-445A-415
Sequence 415, Application US/10020445A
Patent No. 6962797
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PLC74
CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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25 PRIOR FILING DATE: 1998-04-30
26 PRIOR APPLICATION NUMBER: 60/084366
27 PRIOR FILING DATE: 1998-05-05
28 PRIOR APPLICATION NUMBER: 60/084414
29 PRIOR FILING DATE: 1998-05-06
30 PRIOR APPLICATION NUMBER: 60/084441
31 PRIOR FILING DATE: 1998-05-06
32 PRIOR APPLICATION NUMBER: 60/084637
33 PRIOR FILING DATE: 1998-05-07
34 PRIOR APPLICATION NUMBER: 60/084639
35 PRIOR FILING DATE: 1998-05-07
36 PRIOR APPLICATION NUMBER: 60/084640
37 PRIOR FILING DATE: 1998-05-07
38 PRIOR APPLICATION NUMBER: 60/084598
39 PRIOR FILING DATE: 1998-05-07
40 PRIOR APPLICATION NUMBER: 60/084600
41 PRIOR FILING DATE: 1998-05-07
42 PRIOR APPLICATION NUMBER: 60/084627
43 PRIOR FILING DATE: 1998-05-07
44 PRIOR APPLICATION NUMBER: 60/084643
45 PRIOR FILING DATE: 1998-05-07
46 PRIOR APPLICATION NUMBER: 60/085339
47 PRIOR FILING DATE: 1998-05-13
48 PRIOR APPLICATION NUMBER: 60/085338
49 PRIOR FILING DATE: 1998-05-13
50 PRIOR APPLICATION NUMBER: 60/085323
51 PRIOR FILING DATE: 1998-05-13
52 PRIOR APPLICATION NUMBER: 60/085582
53 PRIOR FILING DATE: 1998-05-15
54 PRIOR APPLICATION NUMBER: 60/085700
55 PRIOR FILING DATE: 1998-05-15
56 PRIOR APPLICATION NUMBER: 60/085689
57 PRIOR FILING DATE: 1998-05-15
58 PRIOR APPLICATION NUMBER: 60/085579
59 PRIOR FILING DATE: 1998-05-15
60 PRIOR APPLICATION NUMBER: 60/085580
61 PRIOR FILING DATE: 1998-05-15
62 PRIOR APPLICATION NUMBER: 60/085573
63 PRIOR FILING DATE: 1998-05-15
64 PRIOR APPLICATION NUMBER: 60/085704
65 PRIOR FILING DATE: 1998-05-15
66 PRIOR APPLICATION NUMBER: 60/085697

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Db      7  SLULLFLASHCCIGSARGFLFG-QPDSYKRSNCKP-----IPVNIQLCGHIEYQWRL 60
QY      74  PNLHESHSIAEYKQAQSSMLPLRLARCSHSDPQVLCSPFAPVC---LDRPIYPRRSCEA 130
Db      61  PNLHGHTKMEYVEQAGWIPLMYQKCHPDTKKFLCSFAFVCLDDDETIQCHSLCVQ 120
QY      131 VRACGAPLMEAYGFPPMEHLCHKRPLPNDLCIAVQFQH--LPAT--APPYTKIAOCSEM 186
Db      121 VKORCAPVMSARGFPMPDMLECDRRPQNDLCIPLASDHLLPMTBEAR---KYCEACGN 177
QY      187 EHSADG-LMEQWSSSDVFVQKRIKIKIENGRKILGAQKKKLLKGPRLKRYDTKLYL 245
Db      178 KNDDDMDIMETLCKNDPALKIKVKIKIITYINDTKILLETSKTIYKNGVSRDLKKSVL 237
QY      246 HMGNGAGCCPOLDSIAGSFLVMGKRVNGOLLMAVVRDKNGKEMK 292
Db      238 WLKDSIQCTCEBKNNDINAPLYMGKQGGELVITSYKRWQKQGRBPK 284

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Search completed: March 22, 2006, 22:43:55
Job time : 48 secs

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	Best Local Similarity	43.6%;	Pred. No. 1.6e-62;		
	Matches 125;	Conservative	50;	Indels	17; Gaps 7.
Oy	14	ALALLGLHNAAPRCEBYDYWGQAELHGHSYSKPCQCLDIPADLPLCHTVGKKRRRL	73		
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Db      7  SLULLFLASHCCIGSARGFLFG-QPDSYKRSNCKP-----IPVNIQLCGHIEYQWRL 60
QY      74  PNLHESHSIAEYKQAQSSMLPLRLARCSHSDPQVLCSPFAPVC---LDRPIYPRRSCEA 130
Db      61  PNLHGHTKMEYVEQAGWIPLMYQKCHPDTKKFLCSFAFVCLDDDETIQCHSLCVQ 120
QY      131 VRACGAPLMEAYGFPPMEHLCHKRPLPNDLCIAVQFQH--LPAT--APPYTKIAOCSEM 186
Db      121 VKORCAPVMSARGFPMPDMLECDRRPQNDLCIPLASDHLLPMTBEAR---KYCEACGN 177
QY      187 EHSADG-LMEQWSSSDVFVQKRIKIKIENGRKILGAQKKKLLKGPRLKRYDTKLYL 245
Db      178 KNDDDMDIMETLCKNDPALKIKVKIKIITYINDTKILLETSKTIYKNGVSRDLKKSVL 237
QY      246 HMGNGAGCCPOLDSIAGSFLVMGKRVNGOLLMAVVRDKNGKEMK 292
Db      238 WLKDSIQCTCEBKNNDINAPLYMGKQGGELVITSYKRWQKQGRBPK 284

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Search completed: March 22, 2006, 22:43:55
Job time : 48 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:43:17 ; Search time 165 seconds
(without alignments)
802.739 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAGCVRTALALLG.....MFSYCSLYPPFGAEPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1730	100.0	317	4	US-10-146-474-6 Sequence 6, Appl1
2	1730	100.0	317	4	US-10-338-604-2 Sequence 2, Appl1
3	1730	100.0	317	4	US-10-301-764-6 Sequence 6, Appl1
4	1730	100.0	317	5	US-10-768-566-1 Sequence 1, Appl1
5	1613	93.2	314	4	US-10-338-604-5 Sequence 5, Appl1
6	924.5	53.4	314	4	US-10-146-474-7 Sequence 7, Appl1
7	924.5	53.4	314	4	US-10-138-434A-3 Sequence 3, Appl1
8	924.5	53.4	314	4	US-10-101-764-7 Sequence 7, Appl1
9	924.5	53.4	314	4	US-10-666-851-2 Sequence 2, Appl1
10	924.5	53.4	314	4	US-10-788-792-148 Sequence 148, App
11	924.5	53.4	314	5	US-10-756-149-5611 Sequence 5611, Ap
12	917	53.0	313	4	US-10-425-586-3 Sequence 3, Appl1
13	917	53.0	313	4	US-10-425-586-3 Sequence 3, Appl1
14	917	53.0	338	4	US-10-425-586-4 Sequence 4, Appl1
15	917	53.0	338	4	US-10-425-586-4 Sequence 4, Appl1
16	915	52.9	313	3	US-09-796-008-2 Sequence 2, Appl1
17	915	52.9	313	4	US-10-138-434A-4 Sequence 4, Appl1
18	915	52.9	313	4	US-10-666-851-7 Sequence 7, Appl1
19	915	52.9	313	4	US-10-786-720-43 Sequence 43, Appl1
20	915	52.9	313	5	US-10-817-525-2 Sequence 2, Appl1
21	915	52.9	313	5	US-10-847-972-77 Sequence 77, Appl1
22	903	52.2	314	5	US-10-847-972-80 Sequence 80, Appl1
23	714	41.3	267	4	US-10-425-586-7 Sequence 7, Appl1
24	714	41.3	267	4	US-10-466-136-7 Sequence 7, Appl1
25	659	38.1	246	4	US-10-425-586-6 Sequence 6, Appl1
26	659	38.1	246	4	US-10-466-136-6 Sequence 6, Appl1
27	620.5	35.9	295	3	US-09-934-483A-1 Sequence 1, Appl1

28	620.5	35.9	295	3	US-09-934-483A-5	Sequence 5, Appl1
29	620.5	35.9	295	5	US-10-847-972-81	Sequence 81, Appl1
30	620.5	35.9	295	5	US-10-432-256-5	Sequence 5, Appl1
31	617.5	35.7	295	4	US-10-146-474-2	Sequence 2, Appl1
32	617.5	35.7	295	4	US-10-301-764-2	Sequence 2, Appl1
33	614.5	35.5	295	2	US-08-949-904-2	Sequence 2, Appl1
34	614.5	35.5	295	4	US-10-177-293-142	Sequence 142, App
35	614.5	35.5	295	4	US-10-295-027-1345	Sequence 1345, App
36	614.5	35.5	295	5	US-10-783-528-107	Sequence 107, App
37	614.5	35.5	295	5	US-10-847-972-78	Sequence 78, Appl1
38	614.5	35.5	295	5	US-10-432-256-2	Sequence 2, Appl1
39	614	35.5	275	2	US-08-949-904-3	Sequence 3, Appl1
40	610.5	35.3	295	3	US-09-978-295A-415	Sequence 415, App
41	610.5	35.3	295	3	US-09-978-697-415	Sequence 415, App
42	610.5	35.3	295	3	US-09-978-192A-415	Sequence 415, App
43	610.5	35.3	295	3	US-09-999-832A-415	Sequence 415, App
44	610.5	35.3	295	3	US-09-978-188-415	Sequence 415, App
45	610.5	35.3	295	3	US-09-978-608A-415	Sequence 415, App

ALIGNMENTS

RESULT 1
US-10-146-474-6
; Sequence 6, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Umanaky, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,474
; FILING DATE: 14-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; TELEPHONE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-146-474-6
Query Match 100.0%; Score 1730; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4,66-159;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRAAAGGVTATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPADL 60
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Db 1 MRAAAGGVTATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
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Db 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
QY 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
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Db 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
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Db 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
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Db 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
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Db 301 YPCSLYYPFFYGAAEPH 317

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RESULT 2
US-10-338-604-2
; Sequence 2, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE OF INVENTION: DISORDERS, INCLUDING OBESITY AND DIABETES
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-604-2

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Best Local Similarity 100.0%; Pred. No. 4.6e-169;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAAAGGVTATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPADL 60
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Db 1 MRAAAGGVTATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
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Db 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
QY 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
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Db 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
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Db 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
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Db 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
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Db 301 YPCSLYYPFFYGAAEPH 317

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RESULT 3
US-10-301-764-6
; Sequence 6, Application US/10301764
; Publication No. US20040039184A1
; GENERAL INFORMATION:
; APPLICANT: Umanak, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,764
; FILING DATE: 20-No. US20040039184A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K.
; REGISTRATION NUMBER: 33,943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-301-764-6

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Query Match 100.0%; Score 1730; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.6e-169;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRAAAGGVTATLALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPADL 60
QY 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
   |||
Db 61 PLCHTVGKRMRLPULLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAVCLDRP 120
QY 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
   |||
Db 121 IYPCSLCEAVRAGACAPLMEAYGFPWPEMLHCHKFPLDNDLCIAVQFGLPATAPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
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Db 181 CAQCEMESHADGLMEQCSSDFVVMKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
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Db 241 KRLVLMKNGAGCCPCPQDLSLAGSFLVMGRKYDQGLLMAVYRMDKKNKEMFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
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Db 301 YPCSLYPPFYGAABPH 317

RESULT 4
US-10-768-566-1
; Sequence 1, Application US/10768566
; Publication No. US20040259789A1
; GENERAL INFORMATION:
; APPLICANT: Choudhary, K.
; APPLICANT: Choudhary, K.
; APPLICANT: Ashar, Hena
; APPLICANT: Sayed, Abu
; TITLE OF INVENTION: A METHOD OF TREATING OBESITY AND METABOLIC DISORDERS RELATED TO
; FILE REFERENCE: 69014-B
; CURRENT APPLICATION NUMBER: US/10/768,566
; CURRENT FILING DATE: 2004-01-29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-10-768-566-1

Query Match 100.0%; Score 1730; DB 5; Length 317;
Best Local Similarity 100.0%; Pred. No. 4, 6e-169; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRATLALIGALHMAPARCEYDYGMQAPLHGRSYKPPQCLDIPADL 60
Db 1 MRAAAGGVRATLALIGALHMAPARCEYDYGMQAPLHGRSYKPPQCLDIPADL 60
QY 61 PLCHTYGYKRMRLPNLHESLAEVYQOASSWPLAKRCHSDTQVFLCSLPAVCLDRP 120
Db 61 PLCHTYGYKRMRLPNLHESLAEVYQOASSWPLAKRCHSDTQVFLCSLPAVCLDRP 120
QY 121 IYPCRSLEAVRAGCAPLMEAYGFPWPEMLHCHKPLDNDLCIAVOFGHLPATAPVTKI 180
Db 121 IYPCRSLEAVRAGCAPLMEAYGFPWPEMLHCHKPLDNDLCIAVOFGHLPATAPVTKI 180
QY 181 CAQCEMEHSADGLMEQCSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
Db 181 CAQCEMEHSADGLMEQCSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDY 240
QY 241 KRLVLMKRGAGCPCQDLSLGSFLVMGRKVDGQLLMAVYRWKDKKMKFAVKFMS 300
Db 241 KRLVLMKRGAGCPCQDLSLGSFLVMGRKVDGQLLMAVYRWKDKKMKFAVKFMS 300
QY 301 YPCSLYPPFYGAABPH 317
Db 301 YPCSLYPPFYGAABPH 317

RESULT 5
US-10-338-604-5
; Sequence 5, Application US/10338604
; Publication No. US20030143610A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Haiyan
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF METABOLIC
; FILE REFERENCE: MP101-250P1RM
; CURRENT APPLICATION NUMBER: US/10/338,604
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/346,523
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatcSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 314
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-338-604-5

Query Match 93.2%; Score 1613; DB 4; Length 314;
Best Local Similarity 94.9%; Pred. No. 4, 9e-157; Indels 0; Gaps 0;
Matches 295; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 7 AGVATTAALALIGALHMAPARCEYDYGMQAPLHGRSYKPPQCLDIPADLPLCHTV 66
Db 4 AMSARTTAALALIGALHMAPARCEYDYGMQAPLHGRSYKPPQCLDIPADLPLCHTV 63
QY 67 GYKRMRLPNLHESLAEVYQOASSWPLAKRCHSDTQVFLCSLPAVCLDRPYPKRS 126
Db 64 GYKRMRLPNLHESLAEVYQOASSWPLAKRCHSDTQVFLCSLPAVCLDRPYPKRS 123
QY 127 LCEAVRAGCAPLMEAYGFPWPEMLHCHKPLDNDLCIAVOFGHLPATAPVTKIQAQCEM 186
Db 124 LCEAVRAGCAPLMEAYGFPWPEMLHCHKPLDNDLCIAVOFGHLPATAPVTKIQAQCEM 183
QY 187 EHSADGLMEQCSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYRLVYLH 246
Db 184 EHSADGLMEQCSDFVVKRIKEIKIENGDRKLIQAOKKKLLKPGPLKRDYRLVYLH 243
QY 247 MKNAGCPCQDLSLGSFLVMGRKVDGQLLMAVYRWKDKKMKFAVKFMSYPCSLY 306
Db 244 MKNAGCPCQDLSLGSFLVMGRKVDGQLLMAVYRWKDKKMKFAVKFMSYPCSLY 303
QY 307 YPCSLYPPFYGAABPH 317
Db 304 YPCSLYPPFYGAABPH 314

RESULT 6
US-10-146-474-7
; Sequence 7, Application US/10146474
; Publication No. US20030023061A1
; GENERAL INFORMATION:
; APPLICANT: Melkonian, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES, PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,474
; FILING DATE: 14-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-146-474-7

Query Match          53.4%; Score 924.5; DB 4; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY      1 MRAAAGAGVTAALAL--LGAALHMAPARCEBYDYGMQAE--PLH-GRSYKRPQCLD 55
DB      1 MGIGSEGGRRGAGLGVLLALGALLAVGASAEVDYVFGQDIDGYGSGRRYTKRPQCLD 60
QY      56 IPADLPPLCHTYGYKRMRLPNLLEHESLAEVYQOASSWPLPLAKCHSDTOVFLCSLPAV 115
DB      61 IPADLRLLCHNHYKKMVLPNLLEHETMAEYVQOASSWPLPLLNKCHACTOYVFLCSLPAV 120
QY      116 CLDRPIYCGRSLSCEAVRAGCAPLMEAYGFPMPMEHLGHKFPDLNDLCIAVQFGH-LPATA 174
DB      121 CLDRPIYCGRMVCEAVRSDCEPVMQFFGFYPMELKCDKP-EGVVCIAIMPPTASK 179
QY      175 PPVTYKCAQCMEHSADLMEQMSDSDVNVKRIKEIKIENGDRKLIGAOKKKLLRGP 234
DB      180 PGGTIVGPRCCNELKSEAIIEHLCSSEFALMKIKYKENGDKKIV--PKKKRPLKGP 237
QY      235 LKKRDKRLVLMKXGACGCPQDLSLGSFLVNGRKVDGGLLMAVYMDKKKEMKFA 294
DB      238 IKKDKLKLIVYLKNGADCPCHQDNLNHHFLIMGRKVKSYLLTALIHMDKKKKEFKNF 297
QY      295 VKFMFSYPCSLYYPFF 310
DB      298 MKKMKNHCEPTFGSYV 313

RESULT 7
US-10-138-434A-3
; Sequence 3, Application US/10138434A
; Publication No. US20030175864A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN FRP AND FRAGMENTS THEREOF
; FILE REFERENCE: 4239-62520
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/10/138,434A
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: US 60/050,495
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: US 60/050,417
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-434A-3

Query Match          53.4%; Score 924.5; DB 4; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY      1 MRAAAGAGVTAALAL--LGAALHMAPARCEBYDYGMQAE--PLH-GRSYKRPQCLD 55
DB      1 MGIGSEGGRRGAGLGVLLALGALLAVGASAEVDYVFGQDIDGYGSGRRYTKRPQCLD 60
QY      56 IPADLPPLCHTYGYKRMRLPNLLEHESLAEVYQOASSWPLPLAKCHSDTOVFLCSLPAV 115
DB      61 IPADLRLLCHNHYKKMVLPNLLEHETMAEYVQOASSWPLPLLNKCHACTOYVFLCSLPAV 120
QY      116 CLDRPIYCGRSLSCEAVRAGCAPLMEAYGFPMPMEHLGHKFPDLNDLCIAVQFGH-LPATA 174
DB      121 CLDRPIYCGRMVCEAVRSDCEPVMQFFGFYPMELKCDKP-EGVVCIAIMPPTASK 179
QY      175 PPVTYKCAQCMEHSADLMEQMSDSDVNVKRIKEIKIENGDRKLIGAOKKKLLRGP 234
DB      180 PGGTIVGPRCCNELKSEAIIEHLCSSEFALMKIKYKENGDKKIV--PKKKRPLKGP 237
QY      235 LKKRDKRLVLMKXGACGCPQDLSLGSFLVNGRKVDGGLLMAVYMDKKKEMKFA 294
DB      238 IKKDKLKLIVYLKNGADCPCHQDNLNHHFLIMGRKVKSYLLTALIHMDKKKKEFKNF 297
QY      295 VKFMFSYPCSLYYPFF 310
DB      298 MKKMKNHCEPTFGSYV 313

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Db      61  IPADRLCHNVGYKKMVLPNLLEHETMAEVKQASNVPLLNKKCHAGTQVFLCSLPAPV 120
QY      116  CLDRPIYPCGSLCAVPAAGCAPLMEAYGPPWPEMLHCHKPFLNDLCTAVOGH-LPATA 174
Db      121  CLDRPIYPCGSLCAVPAAGCAPLMEAYGPPWPEMLHCHKPFLNDLCTAVOGH-LPATA 179
QY      175  PEPVRIKACQCEMEHSADGIMQWCSPPFVVMRIKIKIENGDRKLGAOKKKLLKXGP 234
Db      180  PGCTTVCPCDNEIKSEHIEHLCASEFALMKIKYKENGDKKIV--PKKKKPLKGP 237
QY      235  LKRKDTRLVLMKNGAGCCPCPOLDSLASEFLVMGRKVDGQLLMAYVRMDKKKMKFA 294
Db      238  IKKDKLKVLYLKNAGDADPCCHQDLNLSHHFLMIGRKVSQYLLTAIHKMDKKKKEFGNF 297
QY      295  VKEMFSPICSLYPPF 310
Db      298  MKGMKMHCEPTFGSVF 313

RESULT 8
US-10-301-764-7
; Sequence 7, Application US/10301764
; Publication No. US20040039184A1
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & ROEBSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,764
; FILING DATE: 20-No. US20040039184A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018_00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-301-764-7

Query Match      53.4%; Score 924.5; DB 4; Length 314;
Best Local Similarity 56.6%; Pred. No. 3.5e-86;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY      1  MRAAAAAGCVTTAALL--LQALHMAPARCEEYDIYGMQAE--PLH-GNSYSKPPCQD 55
Db      1  MGIRSGSGRGALGVTLALGALLLVGNSASEVDYVSFOSDIDPYSQGRYTRPPCCVD 60

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10 RESULT 10
11 US-10-788-792-148
12 ; Sequence 148, Application US/10788792
13 ; Publication No. US20040191819A1
14 ; GENERAL INFORMATION:
15 ; APPLICANT: Bayer Pharmaceuticals Corporation
16 ; APPLICANT: Eweleigh, Deepa
17 ; APPLICANT: Biswood, Douglas
18 ; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
19 ; FILE REFERENCE: 5152
20 ; CURRENT APPLICATION NUMBER: US/10/788,792
21 ; CURRENT FILING DATE: 2004-02-27
22 ; PRIOR APPLICATION NUMBER: US 60/450,655
23 ; PRIOR FILING DATE: 2003-02-28
24 ; NUMBER OF SEQ ID NOS: 254
25 ; SOFTWARE: PatentIn version 3.2
26 ; SEQ ID NO 148
27 ; LENGTH: 314
28 ; TYPE: PRT
29 ;
30 ;
31 ;
32 ;
33 ;
34 ;
35 ;
36 ;
37 ;
38 ;
39 ;
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Query Match	53.4%;	Score 924.5;	DB 4;	Length 314;
Best Local Similarity	56.6%;	Pred. No. 3.5e-86;		
Matches 179;	Conservative	51;	Mismatches 77;	Indels 9; Gaps 6
QY	1	MRAAAAGVTAATATL--TGALHWAPARCEYDYGMQAE--PLH-GRSYKPPQCID	55	
		1 MGIRSEGGRRGALGVLLALGALLAVGASBYDYVSFGQDIGHYQSGRFYTKPPQCID	60	
Db				
QY	56	IPADLPFLCHTYGYYKRMKLPNLLHEHSIAEVYQOASSWMLPLAKCHSTQVTFCLSPFV	115	
Db	61	IPADLRICHNVYKRYKWLPNLLHEHTAIEVYQOASSWMLPLNKKCHASTQVTFCLSPFV	120	
QY	116	CLDRPIYPCRSITGEAVNAGCAPLMEAYGFPMPBMILHCHKFPDLNDLCAVQFGH-LPATA	174	
Db	121	CLDRPIIYPCRMKLCIAVRDSCSPVWQFPGFTYPMELMKCDKFP-EGDVCIAMTPPNATTSK	179	
QY	175	PPVTKICACQCEMEHSAGLMEQWSSDFVVMRKLEIKIENGDRKLGAQKKKLLKQGP	234	
Db	180	PQGTTCVCPQCNELKSEALIEHLCASEPALMKIKVEYKENGDKITV--PKKKRPLKGP	237	
QY	235	LKKRDTKRLVLAHMKNGAGCCPQDLSLAGSLVWGKRYDQGLLMAATRYWDRKKKEMKFA	294	

```

Db      238  IKKKDLKTLVLYLKNAGADCECHQJLDNLSHHFLINGRKVKSYQLLTALHKKMDKKKEPKNF 297
OY      295  VKFMFSTYPCSLTYFPF 310
          : | : : | :
Db      298  MKKKMKNECPTFQSVF 313

RESULT 11
US-10-756-149-5611
; Sequence 5611, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Azit, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 5611
; LENGTH: 314
; TYPE: PR1
; ORGANISM: Homo Sapiens
US-10-756-149-5611

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; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-425-586-4

```

Query Match	53.0%;	Score 917;	DB 4;	Length 338;
Best Local Similarity	57.9%;	Pred. No. 2.3e-85;		
Matches 179;	Conservative 50;	Mismatches 70;	Indels 10;	Gaps 7

Qy	8	GGVATATALLICATMAPAR--CEBYDYGGQAE--PLH--GRSYKBPQCLDIPALPL	62
Db	8	GGRRGALGVLL-ALGASGRGLGSEYDVVSFQSDIGFYQSGRPFYTKPPQCVDIPADRL	66
Qy	63	CHVYGYRMYLPMYLHESLAEYKQOASRWLPLAKRCHSDPNVQLSLFAPVCLDPRY	122
Db	67	CHVNGYKQWVLPMLHETWAEYKQOASRWPLLNKNGHAGTQVFLCSLFPVCLDPRY	126
Qy	123	PCRSLEAVRAGCAPLMEAYGFPWPEMLCHKFPLDNLCTAVDPGH-LPATAAPVTKIC	181
Db	127	PCRMLCEAVDSCEPVWQFPGFYWPMLKCDKFP--EGDVCIAMTPPNATSKPQFTVC	185
Qy	182	AGCEMHSADGLMEQWSSDPVYVQMKIKETIKILENDRYLIGAKKKLLKGRPLKRDTK	241
Db	186	PCPCNEIKSAILIENHCASEFALRMKIKKKVKNENGKIV--PKKKRKLKGLPKKDKLK	243
Qy	242	RLVYLHMGKAGCCPCPOLDSLAGSLFYVGRKVDGQLLMAVYRWDMKKMKEMKFAVKEFSY	301
Db	244	KLVYLKNGADCFCHQDNLNHHFLIMGRKVSQYLLTALHKMDKNKEPFGMPKKQKNH	303
Qy	302	PCSLIYYPF 310	
Db	304	ECPTFQSVF 312	

```

RESULT 15
US-10-466-136-4
: Sequence 4, Application US/10466136
: Publication No. US20040077828A1
: GENERAL INFORMATION:
: APPLICANT: Rubin, Jeffery et al.,
: TITLE OF INVENTION: SRP AND PEPTIDE MOTIFS THAT INTERACT WITH SRP AND
: TITLE OF INVENTION: METHODS OF THEIR USE
: FILE REFERENCE: 4239-61994
: CURRENT APPLICATION NUMBER: US/10/466,136
: CURRENT FILING DATE: 2003-07-10
: PRIOR APPLICATION NUMBER: US 60/260,908
: PRIOR FILING DATE: 2001-01-10
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 338
: TYPE: PRT
: ORGANISM: Artificial Sequence
FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
: US-10-466-136-4

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Query Match	53.0%	Score 917;	DB 4;	Length 338;
Best Local Similarity	57.9%;	Pred. No. 2.3e-85;		
Matches 179;	Conservative 50;	Mismatches 70;	Indels 10;	Gaps 7

Qy 8 GGVTATLALLGLTHAPAR--CEEEDYGMQAE--PLH--GRSYKSPQCQICDIPADPL 62

Db 8 GGRGALAVTL-ALGASGRGLGSEEDYVSPGSDIGYQSGRPFTTKPQCQICDIPADRL 66

Qy 63 CHYVGRMRLPNTLEHSLAEYKQOASSMLPLARCHSDPQVPLCSLPAPVCLDRPY 122

Db 67 CHNVGKQVLPNTLEHETAEYKQOASSVPLPNTKNCAGVQLCSLPAPVCLDRPY 122

Qy 123 PCRSLEAVRAGCAPLMEAYGFPWPEMLCHFKPLNDNICLVAQGH-LPATAPVYIK 181

Db 127 PCRLTCAVAVDSCEPVNQPGFGYPMELKCDKP-BGDVICAMTPPNTAEASKPGSTVC 185

```

Oy 182 AOCEMESHADGMEOWCSDPFWKORKEIKIENDRKLGAOKKKLLRGPJRKDOTK 2411
Db 186 PBCDNEJCSBAITIEHCASEFMRMRKIKYKKENEDKIV--PKKKPLKGLPKKKDOLK 2433
Oy 242 RLVIHMKNAGCPCPOLDSLAGSPFLWMGRKYDGLLNAVYRMDKKNEMKFAVYEMFSY 3011
Db 244 KLVLYIYNKGNDCPCHQLDNLSHHFLIMGRKYSQYLTLAIIHKMDKKEPFKNPFMKKNKH 3033
Oy 302 PCSLYYPPF 310
Db 304 ECPTFQSVF 312

```

Search completed: March 22, 2006, 22:46:46
Job time : 166 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 22:35:02 ; Search time 187 Seconds
(without alignments)
744.829 Million cell updates/sec

Title: US-10-768-566-1
Perfect score: 1730
Sequence: 1 MRAAAAGCVRTAALALLG.....MFSYPCSLYPPFYGAEPH 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1730	100.0	317	2	AAW37816 Human sec
2	1730	100.0	317	6	ADA38289 Human sec
3	1730	100.0	317	8	ADM67242 Human hom
4	1730	100.0	317	8	ADP56062 Human PRO
5	1733	99.6	317	8	AAW73507 Human ARTS
6	1613	93.2	314	6	ADA38292 Mouse sec
7	1613	93.2	314	8	ADME7241 Murine ad
8	924.5	53.4	314	2	AAW37817 Human sec
9	924.5	53.4	314	2	AAW85528 Human sec
10	924.5	53.4	314	6	ABP72785 Human sec
11	924.5	53.4	314	6	ABP72783 Human sFR
12	924.5	53.4	314	6	ADP68536 Human sec
13	924.5	53.4	314	5	ADR9142 Secreted
14	917	53.0	313	5	ABH82244 Human sec
15	917	53.0	313	8	ADCT1186 Human sec
16	917	53.0	313	8	ADH43308 Human sec
17	917	53.0	338	5	ABH82245 Human sec
18	917	53.0	338	7	ADCT1187 Human sFR
19	917	53.0	338	8	ADH43309 Human sFR
20	916	52.9	362	8	ABM82799 Human dia
21	915	52.9	313	4	AAE10154 Human sec
22	915	52.9	313	4	AAU07695 Human sFR
23	915	52.9	313	6	ABP72784 Human sec
24	915	52.9	313	7	ABR61428 Human emb

25	915	52.9	313	8	ADP68541 Human sec
26	915	52.9	313	8	ADU86503 Human sec
27	915	52.9	313	8	AEA64566 Human lrp
28	915	52.9	313	9	ADV44810 Secreted
29	915	52.9	313	9	ADX58916 Human reg
30	909	52.5	314	7	ABR61429 Murine em
31	903	52.2	314	7	ABR61427 Murine em
32	903	52.2	314	7	ADU86506 Mouse sec
33	714	41.3	267	5	ADH82248 Human sec
34	714	41.3	267	7	ADCT1190 Deletion
35	714	41.3	267	8	ADH43312 Human sec
36	659	38.1	246	5	ABH82247 Human sec
37	659	38.1	246	7	ADCT1189 Deletion
38	659	38.1	246	8	ADH43311 Human sec
39	627	36.2	381	6	ABU55906 Human sFR
40	627	36.2	381	6	ABU55918 Human sec
41	627	36.2	381	6	AAE34072 SRRP 1 pr
42	627	36.2	381	6	AAE34060 FRP prote
43	626	35.9	408	2	AAW74087 Human pro
44	620.5	35.9	295	2	AAW37943 Amino aci
45	620.5	35.9	295	5	ABG31500 Murine se

ALIGNMENTS

RESULT 1	AAW37816	standard, protein, 317 AA.
ID	AAW37816	
AC	AAW37816	
XX		
XX		
DT	28-AUG-1998	(first entry)
XX		
DE	Human secreted apoptosis-related protein hSARP3.	
XX		
KW	Secreted apoptosis-related protein; SARP; hSARP3; human; prostate cancer; breast cancer; diagnosis; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/label= Sig_peptide 29..317
XX		/label= Mat_protein
XX		
PN	WO9813493-A2.	
XX		
PD	02-APR-1998.	
XX		
PF	24-SEP-1997;	97WO-US017154.
XX		
PR	24-SEP-1996;	96US-0026603P.
XX		
PR	11-OCT-1996;	96US-0028363P.
XX		
PA	(LXRB-) LXR BIOTECHNOLOGY INC.	
XX		
PI	Umaneky S, Melkonyan H;	
XX		
DR	WPI: 1998-230704/20.	
DR	N-PsDB; AAV19114.	
XX		
PT	New secreted apoptosis-related proteins - useful for modulating	
PT	apoptosis, particularly for treatment of prostatic or breast cancer, also	
XX	for diagnosis and monitoring of disease.	
PS	Claim 1; Page 56-58; 101pp; English.	
CC	This polypeptide comprises human secreted apoptosis-related protein	
CC	hSARP3 that modulates apoptosis through cell-cell or cell-extracellular	
CC	matrix signalling. Its amino acid sequence was deduced from a clone (see	
CC	AAV19114) obtained from a human pancreas cDNA library. Murine mSARP1 (see	

CC AAW37814), human hSARF1 (see AAW37816) and hSARF2 (see AAW37817) proteins
CC are also claimed. hSARF3 is expressed predominantly in pancreas. SARF
CC polypeptides can be obtained from recombinant host cells. Antibodies
CC specific for SARF polypeptides can be used in immunoassays for detecting
CC levels of expression of SARF, particularly for diagnosis or monitoring of
CC diseases associated with SARF expression. Specifically, they are used to
CC detect cancer of the prostate or breast (by detecting hSARF1 and 2,
CC respectively). SARF polypeptides and nucleic acids can also be used to
CC treat these cancers, or more generally apoptosis-related disease (e.g.
CC infection with HIV or reperfusion injury), also (not claimed) to prevent
CC apoptosis in cultured cells, to improve preservation of organs for
CC transplantation, for in situ preservation for by-pass operations and to
CC treat dermatological disorders. SARF polypeptides can also be used to
CC identify agents, potentially useful therapeutically, that modulate the
CC effects of SARF on mit-1/frizzled protein interaction

XX
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 1730; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-176;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRTRALALLLGALHMAPARCEVDYVGMAEPLHGSRYSKPPQCLDIPADL 60
DB 1 MRAAAGGVRTRALALLLGALHMAPARCEVDYVGMAEPLHGSRYSKPPQCLDIPADL 60
QY 61 PLCHTVGYGRMLPMLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAPVCLDRP 120
DB 61 PLCHTVGYGRMLPMLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAPVCLDRP 120
QY 121 IYPCSLCEAVAVAGCAPLMEAVGFPMPEMLHCHKFPDLNDLCIAVOFGHLPTAPPVTKI 180
DB 121 IYPCSLCEAVAVAGCAPLMEAVGFPMPEMLHCHKFPDLNDLCIAVOFGHLPTAPPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDFVVKRIKEIKIENGRDKLIGAOKKKLLKGPPLKPKDT 240
DB 181 CAQCEMESHADGLMEQCSSDFVVKRIKEIKIENGRDKLIGAOKKKLLKGPPLKPKDT 240
QY 241 KRLVLHMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLHMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
QY 301 YPCSLYYPFFYGABPH 317
DB 301 YPCSLYYPFFYGABPH 317

RESULT 2
ADA38289
ID ADA38289 standard; protein; 317 AA.
XX
XX
AC ADA38289;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted apoptosis related protein (SARF) 3.
XX
XX Human; metabolic disorder; Secreted Apoptosis-Related Proteins 3; SARF3;
KM obesity; overweight; diabetes; insulin resistance; cachexia; anorexia;
KM beta-catenin; leptin; insulin sensitivity; food intake;
KM body weight change; glucose tolerance; hyperplastic growth;
KM cell differentiation; programmed cell death; apoptosis;
KM hypercrophic growth; modulator; agonist; antagonist; antisenese; ribozyme;
KM lipid; glucose; insulin; adipocyte; differentiation; adipose cell;
KM adipocyte; anorectic; antidiabetic; immunomodulator.
XX
OS Homo sapiens.
XX
XX US2003143610-A1.
XX
XX 31-JUL-2003.
XX
XX 08-JAN-2003; 2003US-00338604.
PF

XX
XX 08-JAN-2002; 2002US-0346523P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX
PI Xu H;
XX
DR WPI; 2003-635956/60.
DR N-PSDB; ADA38288, ADA38290.
XX
PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
PT by assaying the ability of the compound to modulate a Secreted Apoptosis-
PT Related Proteins 3 (SARF3) nucleic acid expression or polypeptide
XX activity.
XX
XX Claim 6; SEQ ID NO 2; 35bp; English.
XX
XX The invention discloses a method for identifying a compound for treating
CC a metabolic disorder which comprises assaying the ability of the compound
CC to modulate Secreted Apoptosis-Related Proteins 3 (SARF3) nucleic acid
CC expression or polypeptide activity. Also claimed are methods for
CC modulating SARF3 mediated metabolic activity, treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity and a pharmaceutical formulation for
CC treating metabolic disorders. The metabolic disorders comprise obesity,
CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
CC ability of the compound to modulate SARF3 nucleic acid expression or
CC polypeptide activity is determined by detecting a SARF3 activity of a
CC cell, or by detecting modulation of the level of beta-catenin, leptin or
CC insulin sensitivity, food intake, body weight change, glucose tolerance,
CC hyperplastic growth, cell differentiation, programmed cell death or
CC hypertrophic growth. Modulating SARF3 mediated metabolic activity
CC comprises contacting a cell or tissue expressing the SARF3 with a SARF3
CC modulator. The compound or modulator comprises a small molecule SARF3
CC agonist or antagonist or inverse agonist, anti-SARF3 antibody, antisenese
CC SARF3 molecule or ribozyme. The SARF3 mediated metabolic activity
CC comprises the ability to modulate lipid, glucose or insulin metabolism,
CC adipocyte growth, the differentiation of adipose cell progenitors into
CC adipocytes or programmed cell death. Treating a subject having a
CC metabolic disorder characterized by aberrant SARF3 nucleic acid
CC expression or polypeptide activity comprises administering a SARF3
CC modulator. The compound is an oligonucleotide encoding an antisenese or
CC ribozyme molecule that targets SARF3 transcripts and inhibits translation
CC or an oligonucleotide that forms a triple helix with the promoter of the
CC SARF3 gene and inhibits transcription. The sequence presented is the
CC human SARF3 protein.
XX
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 1730; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.5e-176;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRTRALALLLGALHMAPARCEVDYVGMAEPLHGSRYSKPPQCLDIPADL 60
DB 1 MRAAAGGVRTRALALLLGALHMAPARCEVDYVGMAEPLHGSRYSKPPQCLDIPADL 60
QY 61 PLCHTVGYGRMLPMLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAPVCLDRP 120
DB 61 PLCHTVGYGRMLPMLLEHESLAEVKQOASWMLPLAKRCHSDTVFLCSLFAPVCLDRP 120
QY 121 IYPCSLCEAVAVAGCAPLMEAVGFPMPEMLHCHKFPDLNDLCIAVOFGHLPTAPPVTKI 180
DB 121 IYPCSLCEAVAVAGCAPLMEAVGFPMPEMLHCHKFPDLNDLCIAVOFGHLPTAPPVTKI 180
QY 181 CAQCEMESHADGLMEQCSSDFVVKRIKEIKIENGRDKLIGAOKKKLLKGPPLKPKDT 240
DB 181 CAQCEMESHADGLMEQCSSDFVVKRIKEIKIENGRDKLIGAOKKKLLKGPPLKPKDT 240
QY 241 KRLVLHMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLHMKNGAGCPCPOLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300

QY 301 YPCSLYPPFYGAABPH 317
 DB 301 YPCSLYPPFYGAABPH 317

RESULT 3
 ADM67242
 ID ADM67242 standard; protein; 317 AA.

AC ADM67242;
 DT 03-JUN-2004 (first entry)

DE Human homologue of murine adipocyte specific sFRP-5 protein SeqID 604.

KM human; adipocyte specific; adipose tissue; anti-obesity;
 KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KM adipogenesis; hypertension; cardiovascular disease; anorectic;
 KM antidiabetic; hypotensive; sFRP-5.

OS Homo sapiens.

PN WO2004011618-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023684.

PR 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.

PA (HMGSE-) HMGSE INC.

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66969.

PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.

PS Disclosure; SEQ ID NO 604; 91pp; English.

CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 317 AA;

Query Match 100.0%; Score 1730; DB 8; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.5e-176;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAAAGGVRATALLGALHWAPARCEYDYQWQABPLHGRSYKPPQCLDIPADL 60
 DB 1 MRRAAAGGVRATALLGALHWAPARCEYDYQWQABPLHGRSYKPPQCLDIPADL 60

QY 61 PLCHTVGYKRMRLPMLLEHSLAEVYKQASSMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
 DB 61 PLCHTVGYKRMRLPMLLEHSLAEVYKQASSMLPLAKRCHSDTQVFLCSLFAVCLDRP 120
 QY 121 IYPCRSILCEAVRAGCAPLMEAYGFPPWPMHCHKEPLDNDLCIAVQGHLPATAPVTKI 180
 DB 121 IYPCRSILCEAVRAGCAPLMEAYGFPPWPMHCHKEPLDNDLCIAVQGHLPATAPVTKI 180
 QY 181 CAQCEMEHSADGLMEOWMSSDPVVMRKIKETIENGDKLLGAQKKKLLRGPVKRDT 240
 DB 181 CAQCEMEHSADGLMEOWMSSDPVVMRKIKETIENGDKLLGAQKKKLLRGPVKRDT 240
 QY 241 KRLVLMKNGAGCPCPQDLSLAGSFLVWGRKYDQGLLMAVYRMDKKNKKFAVKFMFS 300
 DB 241 KRLVLMKNGAGCPCPQDLSLAGSFLVWGRKYDQGLLMAVYRMDKKNKKFAVKFMFS 300
 QY 301 YPCSLYPPFYGAABPH 317
 DB 301 YPCSLYPPFYGAABPH 317

RESULT 4
 ADP56062
 ID ADP56062 standard; protein; 317 AA.

AC ADP56062;

DT 18-NOV-2004 (first entry)

DE Human PRO protein sequence SEQ ID NO:2038.

KM human; PRO; immune related disease; inflammatory immune response;
 KM immune response stimulation; anti-allergic; anti-anemic; anti-arthritic;
 KM antiasthmatic; antidiabetic; antiinflammatory; antipruritic;
 KM antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
 KM haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
 KM nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
 KM viricide; gene therapy.

OS Homo sapiens.

PN WO2004039956-A2.

PD 13-MAY-2004.

PF 28-OCT-2003; 2003WO-US034381.

PR 29-OCT-2002; 2002US-0422472P.

PA (GETH) GENENTECH INC.

PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

PI Wood WT, Wu TD;

DR WPI; 2004-376182/35.

DR N-PSDB; ADP56061.

PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
 PT and treating an immune related disease, e.g. systemic lupus
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
 PT stimulating an immune response.

PS Claim 1; SEQ ID NO 2038; 3009pp; English.

CC The present invention describes an isolated PRO nucleic acid (1). Also
 CC described: (1) a vector comprising (1); (2) a host cell comprising the
 CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
 CC antibody which specifically binds to a polypeptide of (4); (7) a
 CC composition of matter comprising a polypeptide of (4), an agonist or
 CC antagonist of the polypeptide or an antibody that binds to the

CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianemic, antiarthritic,
CC antidiabetic, antidiarrhetic, antineoplastic, antiparasitic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC neoplastic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virocidic activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO protein from the present invention.

SQ Sequence 317 AA;

Query Match 100.0%; Score 1730; DB 8; Length 317;

Best Local Similarity 100.0%; Pred. No. 2.5e-176; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAAGGVRRTAALALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPDL 60
DB 1 MRAAAGGVRRTAALALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPDL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
QY 121 IYPCRSLSCEAVRAGCAPLMEAYGFPPWEMLHCHKRPDLNDLCIAVQFGLPATAPVTXI 180
DB 121 IYPCRSLSCEAVRAGCAPLMEAYGFPPWEMLHCHKRPDLNDLCIAVQFGLPATAPVTXI 180
QY 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLKRDY 240
DB 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLKRDY 240
QY 241 KRLVLMHMGKAGCPCPQDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLMHMGKAGCPCPQDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 5

AAW73507 standard; protein; 317 AA.

AAW73507;

01-MAR-1999 (first entry)

Human ATG-1709 protein.

Human; ATG-1709 protein; secreted ligand; 7-Transmembrane receptor;
heart disease; hypertension; cardiovascular disease; kidney disease;
obesity; insulin resistance; diabetes; Central Nervous System disorder;
therapy; sFRP-1.

Homo sapiens.

EP879885-A1.

25-NOV-1998.

16-JAN-1999; 98BP-00300313.

XX 23-MAY-1997; 97US-0047691P.
PR 08-AUG-1997; 97US-00907808.
XX (SMK) SMITHKLINE BEECHAM CORP.

Hu E, Zhu Y;

WPI; 1998-596877/51.

N-PSDB; AAV08946.

New human secreted protein ATG-1709 polypeptide and polynucleotide -

PT useful as diagnostic reagents and for diagnosing, prevention and

PT treatment of Central Nervous System diseases and diabetes.

Claim 11; Page 6; 28pp; English.

CC This sequence represents the human ATG-1709 protein of the invention. ATG
CC -1709 is related to human secreted ligands for 7-Transmembrane receptors
CC and similar to murine sFRP-1. ATG-1709 polypeptides and polynucleotides
CC are useful for diagnosing susceptibility to diseases by detecting
CC mutations in the ATG-1709 gene using probes containing the ATG-1709
CC nucleotide sequence, and can diagnose diseases associated with ATG-1709
CC imbalance by determining ATG-1709 polypeptide expression levels. ATG-1709
CC polypeptides can be used to screen for agonists and antagonists which
CC bind the ATG-1709 polypeptide. These can be used in treatment to activate
CC or inhibit ATG-1709 activity, in addition to direct administration of
CC antisense sequences to prevent expression, or ATG-1709 polypeptides to
CC treat conditions associated with a lack of ATG-1709. Gene therapy may
CC also be used to affect endogenous ATG-1709 expression. ATG-1709
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating ATG-1709 clones or purifying the
CC polypeptides by affinity chromatography. ATG-1709 polypeptides can be
CC administered directly or as a vaccine to inoculate against disease.
CC diseases diagnosed, prevented or treated include: heart disease;
CC hypertension; cardiovascular diseases; kidney diseases; obesity; insulin
CC resistance; diabetes and Central Nervous System (CNS) diseases. The ATG-
CC 1709 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis

SQ Sequence 317 AA;

Query Match 99.6%; Score 1723; DB 2; Length 317;

Best Local Similarity 99.7%; Pred. No. 1.4e-175; Indels 0; Gaps 0;

Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAAAGGVRRTAALALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPDL 60
DB 1 MRAAAGGVRRTAALALIGALHMAPARCEBYDYGMQAEPLHGRSYSKPQCLDIPDL 60
QY 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
DB 61 PLCHTVGYKRMRLPNLLEHESLAEVKQASSWMLPLAKRCHSDTVFLCSLFAVCLDRP 120
QY 121 IYPCRSLSCEAVRAGCAPLMEAYGFPPWEMLHCHKRPDLNDLCIAVQFGLPATAPVTXI 180
DB 121 IYPCRSLSCEAVRAGCAPLMEAYGFPPWEMLHCHKRPDLNDLCIAVQFGLPATAPVTXI 180
QY 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLKRDY 240
DB 181 CAQCEMEHSADGLMEQMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKPGPLKRDY 240
QY 241 KRLVLMHMGKAGCPCPQDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
DB 241 KRLVLMHMGKAGCPCPQDLSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMKFAVKFMS 300
QY 301 YPCSLYYPFFYGAAEPH 317
DB 301 YPCSLYYPFFYGAAEPH 317

RESULT 6

ADA38292

ID ADA38292 standard; protein; 314 AA.
 XX
 AC ADA38292;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Mouse secreted apoptosis related protein (SARP) 3.
 XX
 KM Mouse; metabolic disorder; Secreted Apoptosis-Related Proteins 3; SARP3;
 KM obesity; overweight; diabetes; insulin resistance; cachexia; anorexia;
 KM beta-catenin; leptin; insulin sensitivity; food intake;
 KM body weight change; glucose tolerance; hyperplastic growth;
 KM cell differentiation; programmed cell death; apoptosis;
 KM hypertrophic growth; modulator; agonist; antagonist; antisense; ribozyme;
 KM lipid; glucose; insulin; adipocyte; differentiation; adipose cell;
 KM adipocyte; anorectic; antidiabetic; immunomodulator.
 XX
 OS Mus musculus.
 XX
 PN US2003143610-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 08-JAN-2003; 2003US-00338604.
 XX
 PR 08-JAN-2002; 2002US-0346523P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Xu H;
 XX
 DR WPI: 2003-635956/60.
 DR N-PSDB; ADA38291, ADA38293.
 XX
 PT Identifying a compound for treating a metabolic disorder, e.g., diabetes
 PT by assaying the ability of the compound to modulate a Secreted Apoptosis-
 PT Related Proteins 3 (SARP3) nucleic acid expression or polypeptide
 PT activity.
 XX
 PS Claim 6; SEQ ID NO 5; 35pp; English.
 XX
 CC The invention discloses a method for identifying a compound for treating
 CC a metabolic disorder which comprises assaying the ability of the compound
 CC to modulate Secreted Apoptosis-Related Proteins 3 (SARP3) nucleic acid
 CC expression or polypeptide activity. Also claimed are methods for
 CC modulating SARP3 mediated metabolic activity, treating a subject having a
 CC metabolic disorder characterised by aberrant SARP3 nucleic acid
 CC expression or polypeptide activity and a pharmaceutical formulation for
 CC treating metabolic disorders. The metabolic disorders comprise obesity,
 CC overweight, diabetes, insulin resistance, cachexia or anorexia. The
 CC ability of the compound to modulate SARP3 nucleic acid expression or
 CC polypeptide activity is determined by detecting a SARP3 activity of a
 CC cell, or by detecting modulation of the level of beta-catenin, leptin or
 CC insulin sensitivity, food intake, body weight change, glucose tolerance,
 CC hyperplastic growth, cell differentiation, programmed cell death or
 CC hypertrophic growth. Modulating SARP3 mediated metabolic activity
 CC comprises contacting a cell or tissue expressing the SARP3 with a SARP3
 CC modulator. The compound or modulator comprises a small molecule SARP3
 CC agonist or antagonist or inverse agonist, anti-SARP3 antibody, antisense
 CC SARP3 molecule or ribozyme. The SARP3 mediated metabolic activity
 CC comprises the ability to modulate lipid, glucose or insulin metabolism,
 CC adipocyte growth, the differentiation of adipose cell progenitors into
 CC adipocytes or programmed cell death. Treating a subject having a
 CC metabolic disorder characterised by aberrant SARP3 nucleic acid
 CC expression or polypeptide activity comprises administering a SARP3
 CC modulator. The compound is an oligonucleotide encoding an antisense or
 CC ribozyme molecule that targets SARP3 transcripts and inhibits translation
 CC or an oligonucleotide that forms a triple helix with the promoter of the
 CC SARP3 gene and inhibits transcription. The sequence presented is the
 CC mouse SARP3 protein.
 XX
 SQ Sequence 314 AA;

Query Match 93.2%; Score 1613; DB 6; Length 314;
 Best Local Similarity 94.9%; Pred. No. 8.6e-164;
 Matches 295; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 7 AGCVRTAALALGLHMAPARCEEDYGGWQAEPLHGRSYSPPOCLDIPADLPICHTV 66
 DB 4 AMSARTAALALGLHGAPTRGQEDYDYGWQAEPLHGRSYSPPOCLDIPADLPICHTV 63
 QY 67 GKRRRLPMLHESLAEVKQOASWPLAKRCHSDPQVFLCSFAPVCLDRPIYPCRS 126
 DB 64 GKRRRLPMLHESLAEVKQOASWPLAKRCHSDPQVFLCSFAPVCLDRPIYPCRS 123
 QY 127 LCEAVRAGCAPLMEAYGFPWPEMLHCKRPPLDNDLCIAVQFGLPATAPVTKICAQCEM 186
 DB 124 LCEARAGCAPLMEAYGFPWPEMLHCKRPPLDNDLCIAVQFGLPATAPVTKICAQCEM 183
 QY 187 EHSADGLMEQWSSDFVVKMRKEIKENGDRKLGAKKKKLLKGPLKRDTRVLH 246
 DB 184 EHSADGLMEQWSSDFVVKMRKEIKENGDRKLGAKKKKLLKGPLKRDTRVLH 243
 QY 247 MNGAGCPCPODLSLAGSFLVMGRKVDQLLMAVYRMDKXKEMKFAVKFMFSYPCSLY 306
 DB 244 MNGASCPPODNDITGSEFLVMGRKVBQULLTAYTRMDKXKEMKFAVKFMFSYPCSLY 303
 QY 307 YPFFYGAAEPH 317
 DB 304 YPFFYGAAEPH 314

RESULT 7
 ID ADM67241
 XX ADM67241 standard; protein; 314 AA.
 XX
 AC ADM67241;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Murine adipocyte specific sFRP-5 protein SeqID 603.
 XX
 KM murine; mouse; adipocyte specific; adipose tissue; anti-obesity;
 KM high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KM adipogenesis; hypertension; cardiovascular disease; anorectic;
 KM antidiabetic; hypotensive; sFRP-5.
 XX
 OS Mus musculus.
 XX
 PN W02004011618-A2.
 PD 05-FEB-2004.
 PF 29-JUL-2003; 2003WO-US0233684.
 XX
 PR 29-JUL-2002; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 PA (HMGE-) HMGENE INC.
 XX
 PI Chada K, Chouinard R, Ashar H, Sayed AMD;
 XX
 DR WPI: 2004-143846/14.
 DR N-PSDB; ADM69368.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 PS Claim 47; SEQ ID NO 603; 91pp; English.
 XX
 CC This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti-
 CC obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and

Query Match	53.4%	Score 924.5	DB 2	Length 314
Best Local Similarity	56.6%	Pred. No. 3,9e-90		
Matches 179	Conservative 51	Mismatches 77	Indels 9	Gaps 6

Query	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
1	M	R	A	A	A	G	G	V	R	T	A	A	L	T	-	-	L	G	A	L	T	A	P	A	R	C	E	E	D	D	Y	Y	G	G	A	A	-	-	P	L	H	-	G	R	S	K	P	Q	C	D	55									
Db	1	M	O	I	G	S	E	G	G	R	R	A	L	C	V	A	L	A	G	A	L	L	A	V	S	A	B	E	D	V	S	T	G	S	D	G	P	G	S	R	F	T	K	P	Q	C	V	D	60											
0	56	I	P	A	D	I	P	L	C	H	T	V	G	Y	K	E	M	R	L	P	N	L	L	E	H	S	L	A	E	V	K	O	A	S	S	W	L	P	L	A	K	R	C	H	S	D	T	Q	V	L	C	S	I	P	A	V	115			

DB	Accession	Score	Length	Matches	Indels	Gaps
Db	IPADRLCHNAVGYKKMVLPIILLHEHTMAEYQASSWPLANKNGHAGTQVFLCSLPAPV	61	120			
Qy	116 CLDRPIYECRSLCEAVRAGCAPLMEAYGFPWPEMLHCHKPFLDNDLCIAVOFGH-LPATA	174				
Db	121 CLDRPIYECRMLCEAVRSCBEPVMQFFGFYPEMLKCKXFP-EGDVCIAMTPPNATEASK	179				
Qy	175 PPVTIKCAQCEMEHSADGLMEQMSCSDPVVKKRIEIKIENGDRKLIGAKKKLLKQEP	234				
Db	180 FQGTIVCPCCNENLKESEAIIIEHLCSSEPALNRKIKVEKKENDKKIV-PPKKKPLKQEP	237				
Qy	235 LKRKDTKRLVYLMKNGAGCCPCPOLDSLAFSPFLWGRKVDGOLLMAVYRWDKGNEMKPA	294				
Db	238 IKKDKLKKLVLYLKNAGADCPCHQDNLNHHFLIMGRKVKYSQYLLPAIHAKMDKKNKEFPKNF	297				
Qy	295 VKFMFSYPCSLYYPF 310					
Db	298 MKGMKHECPTFGSVF 313					
RESULT 10						
ID	ABP72785					
AC	ABP72785 standard; protein; 314 AA.					
XX	ABP72785;					
DT	17-JUN-2003 (first entry)					
XX	Human secreted frizzled related protein.					
DE	Human, secreted frizzled related protein; sFRP, ischaemia; heart disease;					
XX	cardiant; vasotropic; gene therapy.					
OS	Homo sapiens.					
XX	WO2003025152-A2.					
PD	27-MAR-2003.					
PF	23-SEP-2002; 2002WO-US030100.					
XX	21-SEP-2001; 2001US-0323816P.					
PA	(GENE-) GENE LOGIC INC.					
PA	(PROC) PROCTER & GAMBLE CO.					
PI	Einstein R, White M, Bednarik D, Greene J, Doersen C;					
XX	WPI; 2003-342664/32.					
DR	N-PSDB; ABZ82228.					
XX						
PT	New isolated nucleic acid encoding a human secreted frizzled related					
PT	protein, useful for preparing a composition for treating ischemic heart					
XX	disease.					
PS	Claim 1; Page 49-50; 57bp; English.					
CC	The present sequence is the protein sequence of human secreted frizzled					
CC	related protein (sFRP). A variant sFRP protein (see ABP72783) has been					
CC	identified that is associated with ischemic heart disease. The variant					
CC	sequence differs from the present sequence in having Ala substituting for					
CC	Pro at position 174. The invention provides sFRP variant nucleic acids,					
CC	vector, host cells, and methods of producing the variant polypeptide.					
CC	The variant sFRP nucleic acids and polypeptides can be used to identify					
CC	agents which modulate the expression or activity of the polypeptide, to					
CC	identify binding partners for the protein, to raise antibodies, and as					
CC	diagnostic, prognostic and therapeutic agents for ischaemic heart disease					
XX						
XX	Sequence 314 AA;					
Query Match	53.4%; Score 924.5; DB 6; Length 314;					
Best Local Similarity	56.6%; Pred. No. 5.9e-90;					
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6						

Qy 1 MRAAADAAGVRRATALL--LGAHMAAPARCSEYDYYGQAE--PLH-GASYKPPQCLD 55
Db 1 MGIGSEGGRRRAALGVLLATGALLAVGSASASYDVAS:FQSDIGPYQSGSEFYTKPPQCV 60
Qy 56 IPADPLGHTVGYKMYRLPNLLEHESIAEYKQOASMWLPLAKRCHSDTQVFLCSLFAVY 115
Db 61 IPADRLCHNGVYKKQVLPNLLEHETMAEYKQOASMWELPNKNGCIAGTQVFLCSLFAVY 120
Qy 116 CLDRDIYPCRSICEAVRAGCAPLMEAYGFPWPEMLCHKFPLDNDLCIAVQFGH-LPATA 174
Db 121 CLDRITYPGRMICEAVRDSCEPVMQGFPGFWPEMLCKDKFP-EGDYCIANTPNNPTEASK 179
Qy 175 PPVTKYCAQCEMEHSHADGLMEQNCSSDFFVYKRIKIKIETLNGDRKLI GAQKKKKLLKPGP 224
Db 180 PGGTTPVCPDNDLSEALIEHLCASEFPLRMKIKKVKKENGDKKTV--PKKKKPLKGP 237
Qy 225 LKRRKTKLVLMKNGAGGCPQOLDBLASSFLVMGKRVQDGLLMAVYRPDKNKEMKFA 234
Db 238 IKKKDLKTLVLMKNGADPCHQDLNLSHFILMGRKVSQYLLTAIHKDKDKNKPKNF 237
Qy 295 VKFMFSPCGLSYLPFF 310
Db 298 MKGMKNHECPYFQSVF 313

RESULT 11	
ABP72783	
ID	ABP72783 standard; protein, 314 AA.
XX	
AC	ABP72783;
XX	
DT	17-JUN-2003 (first entry)
XX	
DE	Human sFRP variant associated with ischaemia in heart tissue.
XX	
KW	Human; secreted frizzled related protein; sFRP; ischaemia; heart disease;
XX	cardiant; vasotropic; gene therapy.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Misc-difference 13
FT	/note= "absent in wild-type sFRP"
FT	Misc-difference 174
FT	/note= "wild-type Pro substituted by Ala"
XX	
PN	WO2003025152-A2.
XX	
PD	27-MAR-2003.
XX	
PF	23-SEP-2002; 2002WO-US030100.
XX	
PR	21-SEP-2001; 2001US-0323816P.
XX	
PA	(GENE-) GENE LOGIC INC.
PA	(PROC) PROCTER & GAMBLE CO.
XX	
PI	Einstein R, White M, Bednarik D, Greene J, Doersen C;
XX	
WI	PI; 2003-342664/32.
DR	N-PSDB; ABZ82226.
XX	
FT	New isolated nucleic acid encoding a human secreted frizzled related
PT	protein, useful for preparing a composition for treating ischemic heart
PT	disease.
XX	
PS	Disclosure: Page 54-55; 57pp; English.
XX	
CC	The present sequence is the protein sequence of a human secreted frizzled
CC	related protein (sFRP) variant polypeptide that is associated with
CC	ischemic heart disease. Expression of the corresponding mRNA was found
CC	to be decreased in ischemic heart tissue. The variant sequence differs
CC	

from the wild-type sequence in having an additional Ala residue at position 13 and having a Pro to Ala substitution at position 174. The invention provides sFRP variant nucleic acids, vectors, host cells, and methods of producing the variant polypeptide. The variant sFRP nucleic acids and polypeptides can be used to identify agents which modulate the expression or activity of the polypeptide, to identify binding partners for the protein, to raise antibodies, and as diagnostic, prognostic and therapeutic agents for ischaemic heart disease

Query Match	53.4%	Score 924.5;	DB 6;	Length 314;
Best Local Similarity	56.6%	Pred. No. 5.9e-90;		
Matches 179;	Conservative 51;	Mismatches 77;	Indels 9;	Gaps 6

```
QY      1 MRAAAAAGVRTTAAALL--LGAALHMAARCEBYDYDYOQAE--PLH-GRSYSGRPQCID 55
Db      1 MGIGREGGRGGAALGVLLTALGALLAAVGASAEVDYVSPOSIDGRYOSGRFYTKPPQVD 60
QY      56 IPADLPLCHTVGYKGMRLPNLLEHESLAEVYQQAASMWPLTAKRCHSDTOVPLCSLPAPV 115
Db      61 IPADLRICHNVGYKKVRLPNLLEHETVMAEVQQAASMWPLLNKCHAGTOVPLCSLPAPV 120
QY      116 CLDRPIYPCRSICEAVRAGACALYMAEYGFPPMPMLHCHEPLDNLDCIAVOFGH-LPATA 174
Db      121 CLDRPIYPCRMICEAVRDSCBFWQPFQGYPMPLKCDKPF--EGDVCIAMTPPRATASK 179
QY      175 PAVTKICAQCEMEHNSADGLMEQMCSSDVFVKRIKEIKIENGDRKLLGAOKKKKLLKPGP 234
Db      180 PGDTTCPCPDNDMLSEATIEHLGASBEPALMKIKEVKENGDKIY--PRKKKPKLGLP 237
QY      235 LKRKDTKRLVLMKNGAGCPCPOLDLSLGSFLVNGRKVTDGOLLMAVYRMDKKKKEKFA 294
Db      238 IKKKDKLKKVLVYLKNGADPCPQDLNLSHNFELMGIRKVKSGYLLTALTKWDKKKKEKXF 297
QY      295 VKEMFSYPCSLYYPPF 310
Db      298 MKQKKNHECPFQSVF 313
```

```

RESULT 12
ADP68536
ID ADP68536 standard; protein, 314 AA.
XX
XX
AC ADP68536;
XX
XX
DT 09-SEP-2004 (first entry)
XX
DE Human secreted frizzled related protein, sFRP-1.
XX
XX KW bone-formation; secreted frizzled related protein; sFRP; bone disorder;
KW bone formation disorder; bone resorption disorder; bone density disorder;
KW degenerative bone disorder; osteodegeneration disorder; osteopenia;
KW osteoarthritis; osteoporosis; type II osteoporosis; human; sFRP-1.
XX
XX OS Homo sapiens.
XX
XX PN US204115195-A1.
XX
XX PD 17-JUN-2004.
XX
XX PE 19-SEP-2003; 2003US-00666851.
XX
XX PR 31-MAY-2002; 2002US-00169545.
XX PR 19-SEP-2002; 2002US-0412379P.
XX
XX PA (BODI/) BODINE P.
XX
XX PI Boline P;
XX
XX WP1; 2004-449339/42.
XX
XX N-PSDB; ADP68535.
XX

```

PT New compositions comprising secreted frizzled related protein (sFRP),
PT anti-sFRP antibody, nucleic acid encoding sFRP or the antibody, or sFRP
PT antisense nucleic acids, for regulating bone-forming activity or treating
PT bone diseases.

Claim 24; SEQ ID NO 2; 57pp; English.

CC The invention relates to a pharmaceutical composition for regulating bone
CC -forming activity in a mammal comprising at least one a secreted frizzled
CC related protein (sFRP) or its regulating portion, an antibody against
CC such proteins, a nucleic acid that encodes for the protein or antibody,
CC an sFRP antisense nucleic acid, or a small molecule that has an effect on
CC any of the above. The pharmaceutical composition is useful for regulating
CC bone-forming activity in a mammal, or for treating a bone disorder in a
CC human, such as bone formation disorder, bone resorption disorder, a bone
CC density disorder or a degenerative bone disorder, such as an
CC osteodysgenesis disorder, e.g. osteopenia, osteoarthritis, or
CC osteoporosis, specifically type II osteoporosis. The present sequence
CC represents the amino acid sequence of the human secreted frizzled related
CC protein, sFRP-1.

XX Sequence 314 AA;

Query Match 53.4%; Score 924.5; DB 8; Length 314;
Best Local Similarity 56.6%; Pred. No. 5.9e-90;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVTAALAL--LGAALHAPARCEBYDYGMQAE--PLH-GRSYKPPQCLD 55
DB 1 MGIGSEGGRRGAAAGVLLALGALLAVGASBYDYVSFGSDIGPQSGRFTTKPPQCV 60
QY 56 IPADPLCHTVGYGKMRLLPNLEHESLAEVKQOASWMLPLAKRGHSDTVFLCSLFAV 115
DB 61 IPADRLCHNVGYKKMVLPNLEHETMAEVKQOASWVLLNKNCHAGTQVFLCSLFAV 120
QY 116 CLDRPIYPCRSLSCEAVRAGACPLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 174
DB 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFVPEMLKCKDFP-EGDVCIAMTPPNNTASK 179
QY 175 PAVTKICAGCEMEHSDGLMEQSCSDPVVVKRIKIKIENGDRKILGAQKKKLLKPGP 234
DB 180 PGGTVPCPCDNLKSEALIEHLICASEFALRMKIKIVKKEKNDKTIIV--PKKKRPLKIGP 237
QY 235 LKRXDTRKLVLMKNKAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWMDKKNKEMKPA 294
DB 238 IKKKDLKLVLYLKNKAGDCPCQDLDNLSHFLIMGRKVSQYLLTAIHKMDKKKKEPKNF 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKMKMNHCEPTFGSVF 313

RESULT 13
ID ADR99142 standard; protein; 314 AA.

XX ADR99142;
XX 02-DEC-2004 (first entry)
XX Secreted frizzled-related protein 1, sFRP1, SEQ ID 148.
XX
XX Cytostatic; breast cancer; cancer; human;
XX Secreted frizzled-related protein 1; sFRP1.
XX Homo sapiens.
XX
XX WO2004078035-A2.
XX
XX 16-SEP-2004.
XX
XX 27-FEB-2004; 2004WO-US007268.

PR 28-FEB-2003; 2003US-0450655P.

XX (FARB) BAYER PHARM CORP.

XX Eweleigh D. Bigwood D;

XX WPI; 2004-653556/63.

XX N-PsDB; ADR99015.

PT Diagnosing breast cancer comprises comparing the level of expression of
PT genes or gene products in a first biological sample taken from a patient
PT with that in a normal patient sample.

Claim 3; SEQ ID NO 148; 53pp; English.

CC The present invention relates to a method (M1) for diagnosing breast
CC cancer in a patient. The method comprises comparing the level of
CC expression of one or more genes or gene products in a biological sample
CC from the patient with that in a normal patient sample, where a difference
CC in the gene expression in the first sample compared to that in the second
CC sample is a diagnostic of the disease. Also claimed are: method (M2) for
CC distinguishing between normal and disease tissues; method (M3) for
CC monitoring the response of a breast cancer patient to treatment with an
CC anti-cancer agent; method (M4) for identifying a compound for treating
CC breast cancer; and an array for distinguishing between normal and disease
CC tissues comprising two or more probes corresponding to genes selected
CC from ADR98995-ADR99121 or comprising two or more polypeptides selected
CC from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995
CC -ADR99121 and the gene products are polypeptides selected from ADR99122-
CC ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are
CC useful for distinguishing between normal and disease tissue. M3 is useful
CC for monitoring the response of a breast cancer patient to treatment with
CC an anti-cancer agent. M4 is useful for identifying a compound for
CC treating breast cancer. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 314 AA;

Query Match 53.4%; Score 924.5; DB 8; Length 314;
Best Local Similarity 56.6%; Pred. No. 5.9e-90;
Matches 179; Conservative 51; Mismatches 77; Indels 9; Gaps 6;

QY 1 MRAAAGAGVTAALAL--LGAALHAPARCEBYDYGMQAE--PLH-GRSYKPPQCLD 55
DB 1 MGIGSEGGRRGAAAGVLLALGALLAVGASBYDYVSFGSDIGPQSGRFTTKPPQCV 60
QY 56 IPADPLCHTVGYGKMRLLPNLEHESLAEVKQOASWMLPLAKRGHSDTVFLCSLFAV 115
DB 61 IPADRLCHNVGYKKMVLPNLEHETMAEVKQOASWVLLNKNCHAGTQVFLCSLFAV 120
QY 116 CLDRPIYPCRSLSCEAVRAGACPLMEAYGFPWPEMLHCHKFPDNDLCTAVQFGH-LPATA 174
DB 121 CLDRPIYPCRMVCEAVRDSCEPVMOFGFVPEMLKCKDFP-EGDVCIAMTPPNNTASK 179
QY 175 PAVTKICAGCEMEHSDGLMEQSCSDPVVVKRIKIKIENGDRKILGAQKKKLLKPGP 234
DB 180 PGGTVPCPCDNLKSEALIEHLICASEFALRMKIKIVKKEKNDKTIIV--PKKKRPLKIGP 237
QY 235 LKRXDTRKLVLMKNKAGCPCPQDLSLGSFLVMGRKVDGQLLMAVYRWMDKKNKEMKPA 294
DB 238 IKKKDLKLVLYLKNKAGDCPCQDLDNLSHFLIMGRKVSQYLLTAIHKMDKKKKEPKNF 297
QY 295 VKFMFSYPCSLYYPPF 310
DB 298 MKMKMNHCEPTFGSVF 313

RESULT 14
ID ABB82244 standard; protein; 313 AA.

XX ABB82244;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 22:38:37 ; Search time 40 Seconds

(without alignments)
762.518 Million cell updates/sec

Title: US-10-768-566-1

Perfect score: 1730

Sequence: 1 MRAAAGGVRTRALALLG.....MFSYPSLTPFFYGAAEPH 317

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1723	99.6	317	2	frizzled protein-1
2	614.5	35.5	235	2	frizzled protein-2
3	292.5	16.9	574	2	frizzled-7 protein
4	277	16.0	581	2	gene frizzled prot
5	268	15.5	581	2	FZD10 protein - hu
6	266.5	15.4	694	2	wingless receptor
7	263.5	15.2	568	2	frizzled-1 protein
8	262.5	15.2	565	2	frizzled-2 protein
9	262	15.1	647	2	frizzled-1 protein
10	253.5	14.7	537	2	frizzled protein 4
11	247.5	14.3	641	2	probable intercell
12	243	14.0	550	2	wingless protein r
13	206	11.9	666	2	frizzled-3 protein
14	202	11.7	197	2	frizzled-related p
15	198.5	11.5	605	2	hypothetical prote
16	191	11.0	706	2	frizzled-6 protein
17	161	9.3	1113	2	low-density lipopr
18	159.5	9.2	1774	2	collagen alpha 1(X
19	134.5	7.8	579	2	membrane-type friz
20	124	7.2	526	2	frizzled protein h
21	106	6.1	793	2	smoothed protein
22	91	5.3	327	2	hypothetical prote
23	90	5.2	1699	2	complement compone
24	90	5.2	1906	1	myosin-light-chain
25	89	5.1	583	2	alpha, alpha-trehal
26	88	5.1	635	2	probable RNA helic
27	87	5.0	211	1	metalloproteinase
28	86	5.0	784	2	cell division prot
29	85.5	4.9	1050	2	hypothetical prote

30	85	4.9	465	2	ST57564	nifB protein - Ent
31	84.5	4.9	1000	2	JB0110	mitotic control pr
32	84.5	4.9	1365	2	T13991	nucleoporin 154 -
33	84	4.9	713	2	JC2534	RVG protein - rat
34	84	4.9	7463	2	T36248	CDA peptide synth
35	83.5	4.8	211	2	JC4630	metalloproteinase
36	83.5	4.8	1513	2	T23681	hypothetical prote
37	82.5	4.8	211	1	A53532	hypothetical prote
38	82.5	4.8	902	2	B40494	androgen receptor
39	81.5	4.7	892	2	T15195	hypothetical prote
40	81.5	4.7	1322	2	D82685	phosphoribosylform
41	81.5	4.7	1349	2	T13031	nucleoporin - fru
42	81.5	4.7	1608	2	T13216	minor capsid prote
43	81	4.7	195	2	E82090	hypothetical prote
44	81	4.7	306	2	D82126	histone deacetylase
45	81	4.7	442	2	B31249	transforming growt

ALIGNMENTS

RESULT 1
JB0175
frizzled protein-1b - human
C/Species: Homo sapiens (man)
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C/Accession: JB0175
R;Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beely, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A;Reference number: JB0174; MUID:98308108; PMID:9642118
A;Accession: JB0175
A;Molecule type: mRNA
A;Residues: 1-317 <HUA>
A;Cross-references: UNIPROT:O14780; UNIPARC:UPI0000158811
C;GeneID: 8
A;Gene: hFRP-1b
A;Map position: 5q14.3-q12.1

Query Match 99.6%; Score 1723; DB 2; Length 317;
Best Local Similarity 99.7%; Pred. No. 1.9e-147;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MRAAAGGVRTRALALLGALHMAPARCEEYDYGMOAEPHAGRSYKPPQCLDIPADL	60
DB	1	MRAAAGGVRTRALALLGALHMAPARCEEYDYGMOAEPHAGRSYKPPQCLDIPADL	60
QY	61	PLCHTVGYKRMRLPNLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAPVCLDRP	120
DB	61	PLCHTVGYKRMRLPNLEHESLAEVKQOASSWLPILAKRCHSDTQVFLCSLPAPVCLDRP	120
QY	121	TPCRSLCEAVYAGCAPLMEAYGFPWPEMLHCHKRPPLNDLCIAVOFGHLPPTAPPVTKI	180
DB	121	TPCRSLCEAVYAGCAPLMEAYGFPWPEMLHCHKRPPLNDLCIAVOFGHLPPTAPPVTKI	180
QY	181	CAQCEHESADGLMOMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKGPPLKRDY	240
DB	181	CAQCEHESADGLMOMCSSDFVVKRIKEIKIENGDRKLGAQKKKLLKGPPLKRDY	240
QY	241	KRLVLMKNGACPCPQDLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMFAVKFMS	300
DB	241	KRLVLMKNGACPCPQDLDSLAGSFLVMGRKVDGQLLMAVYRMDKKNKEMFAVKFMS	300
QY	301	YPCSLTYPPFYGAABPH 317	
DB	301	YPCSLTYPPFYGAABPH 317	

RESULT 2
JB0174
frizzled protein-2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

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